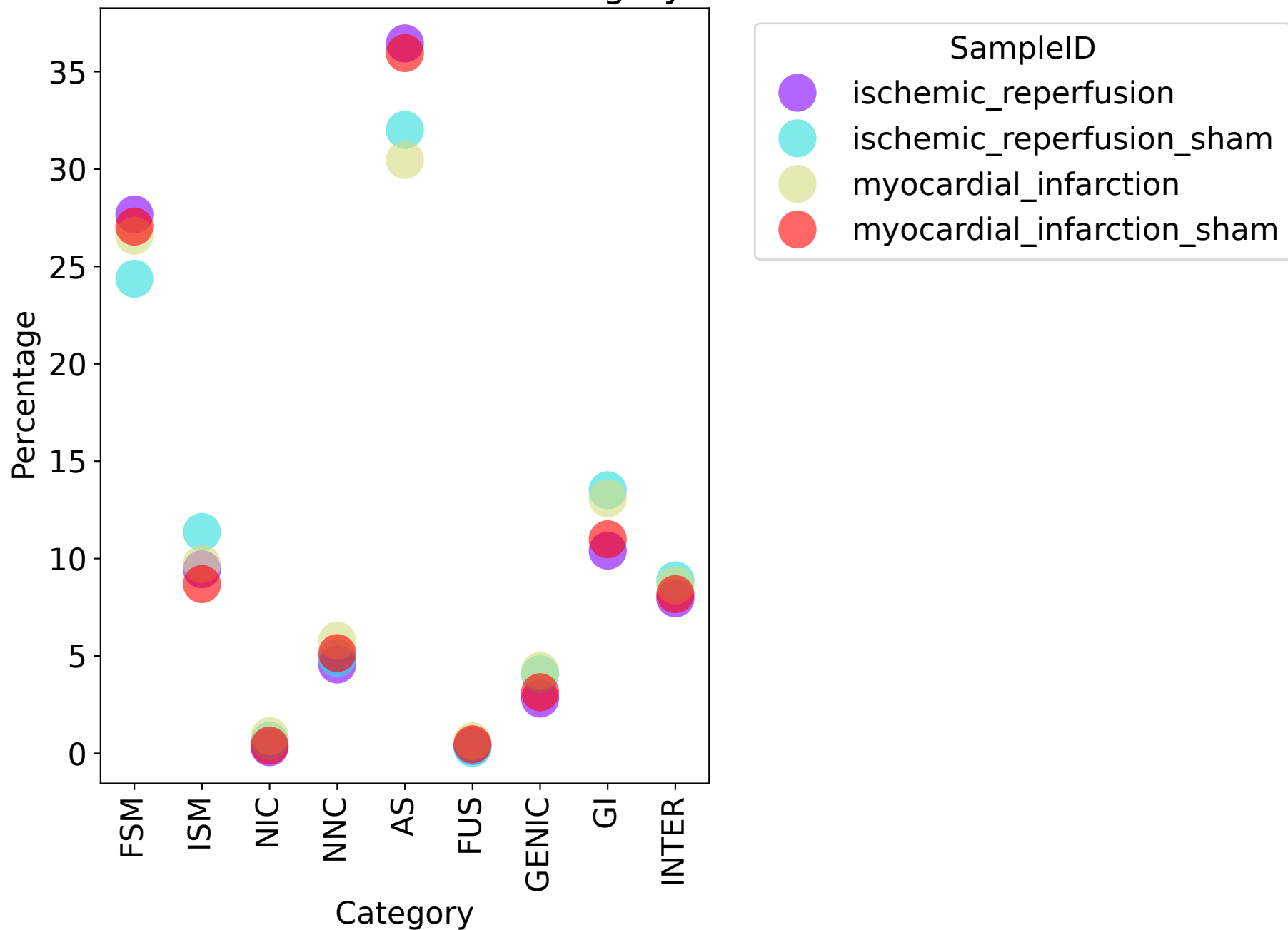
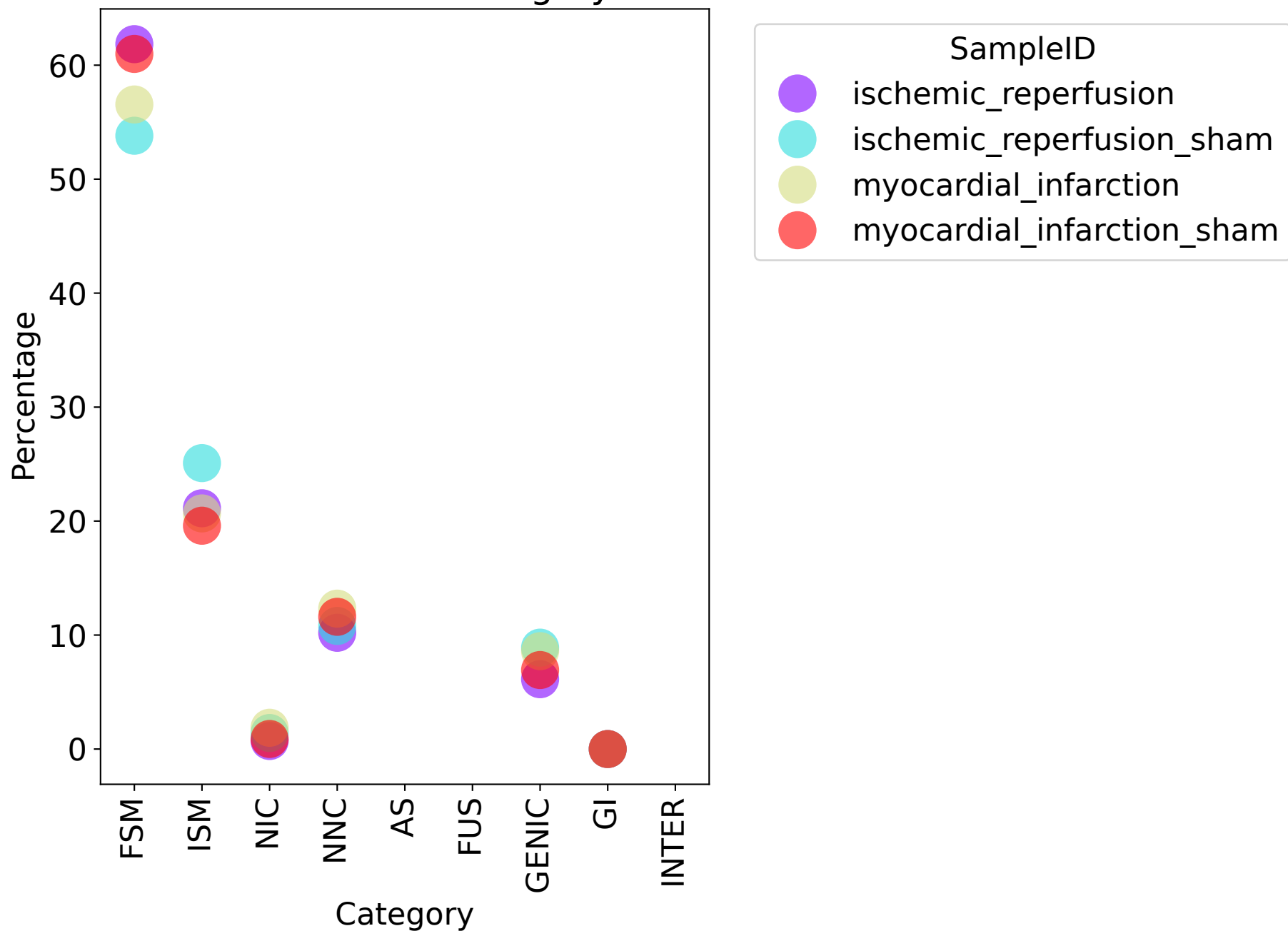


SQANTI-reads report

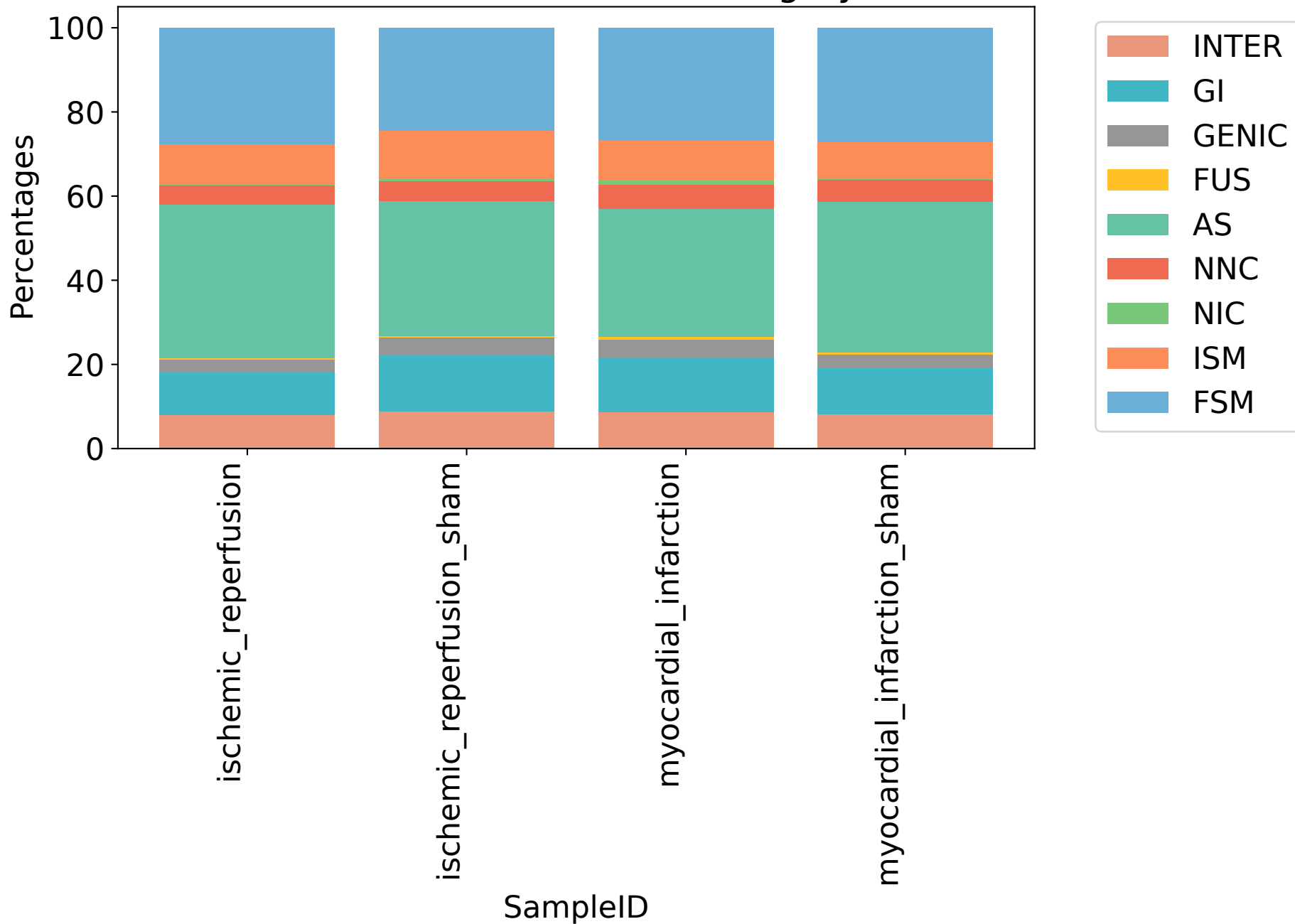
Percent reads in each structural category - All Genes

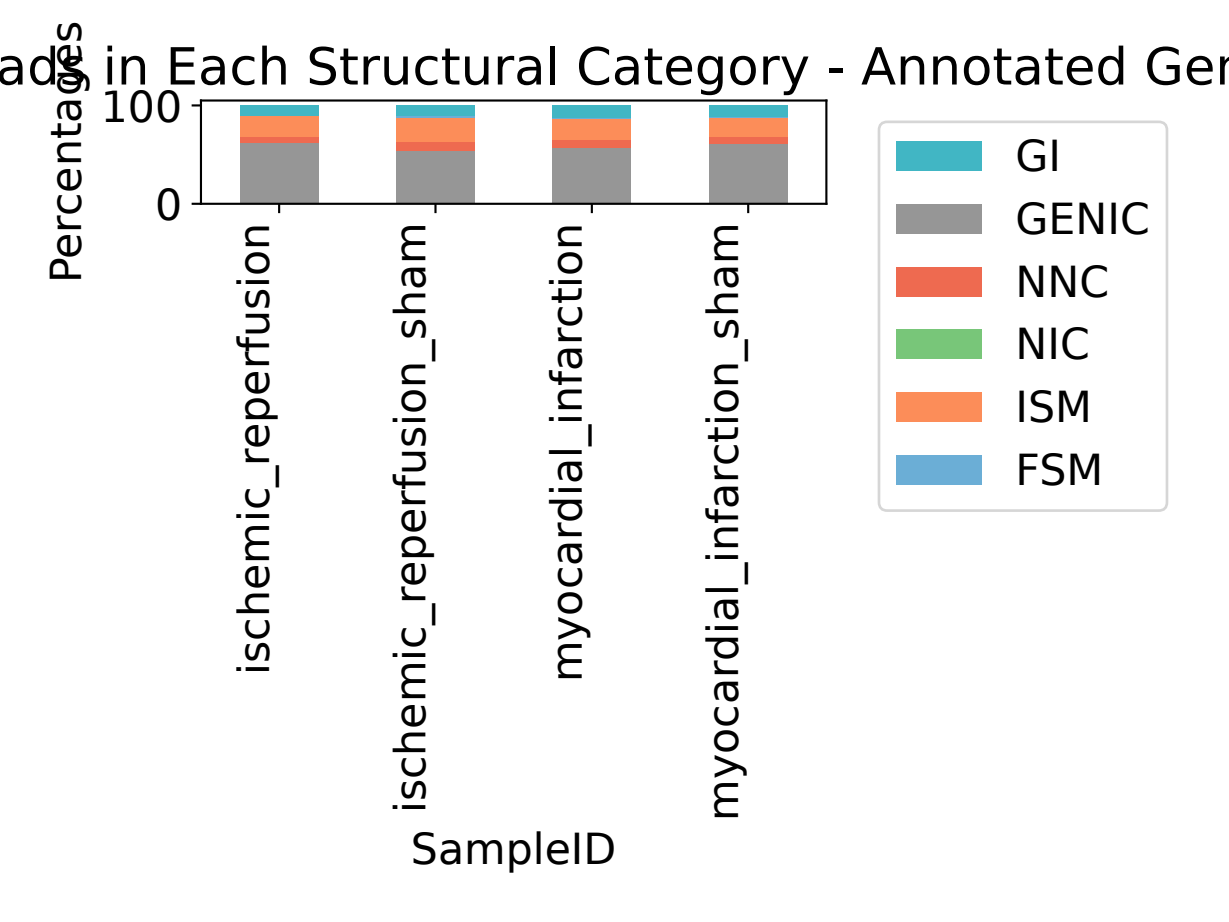


t reads in each structural category - Annotated Genes

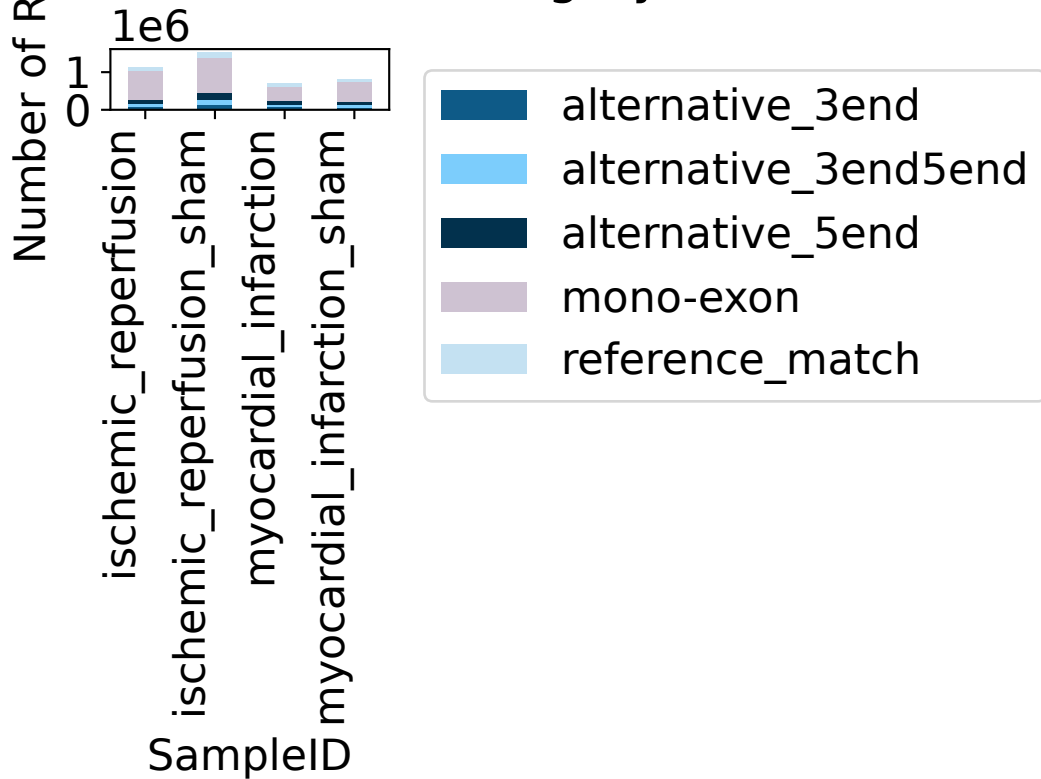


Percent Reads in Each Structural Category - All Genes

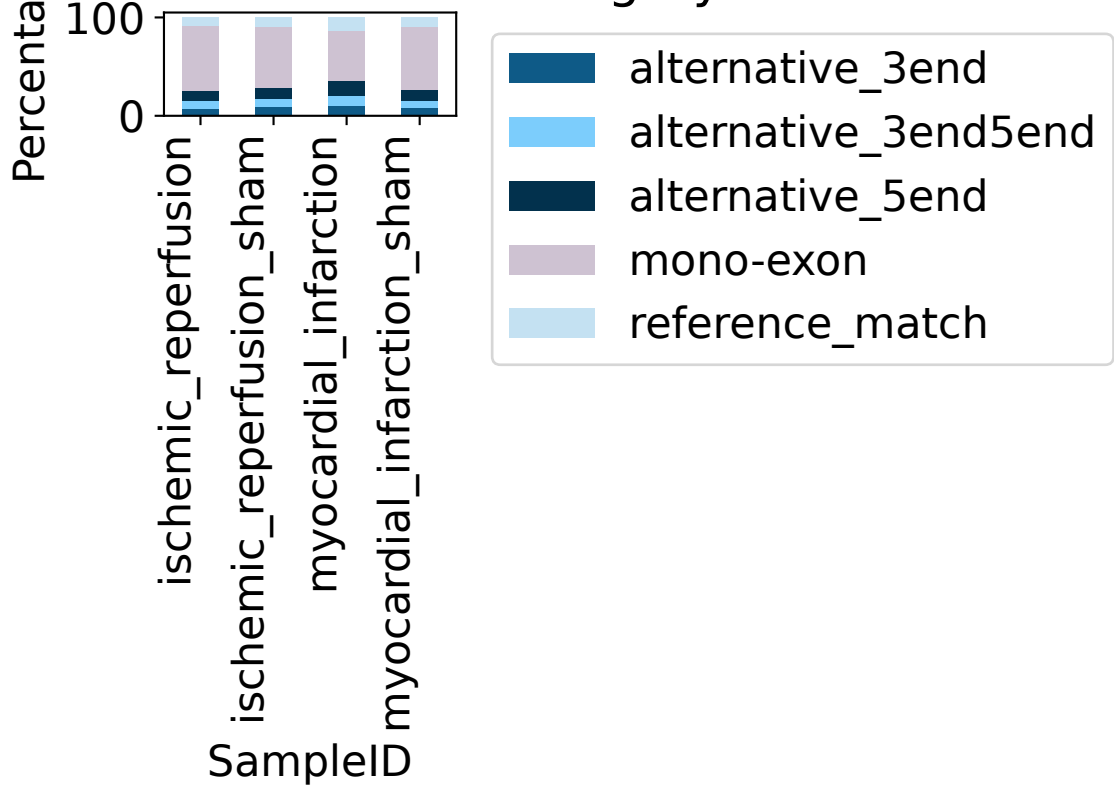




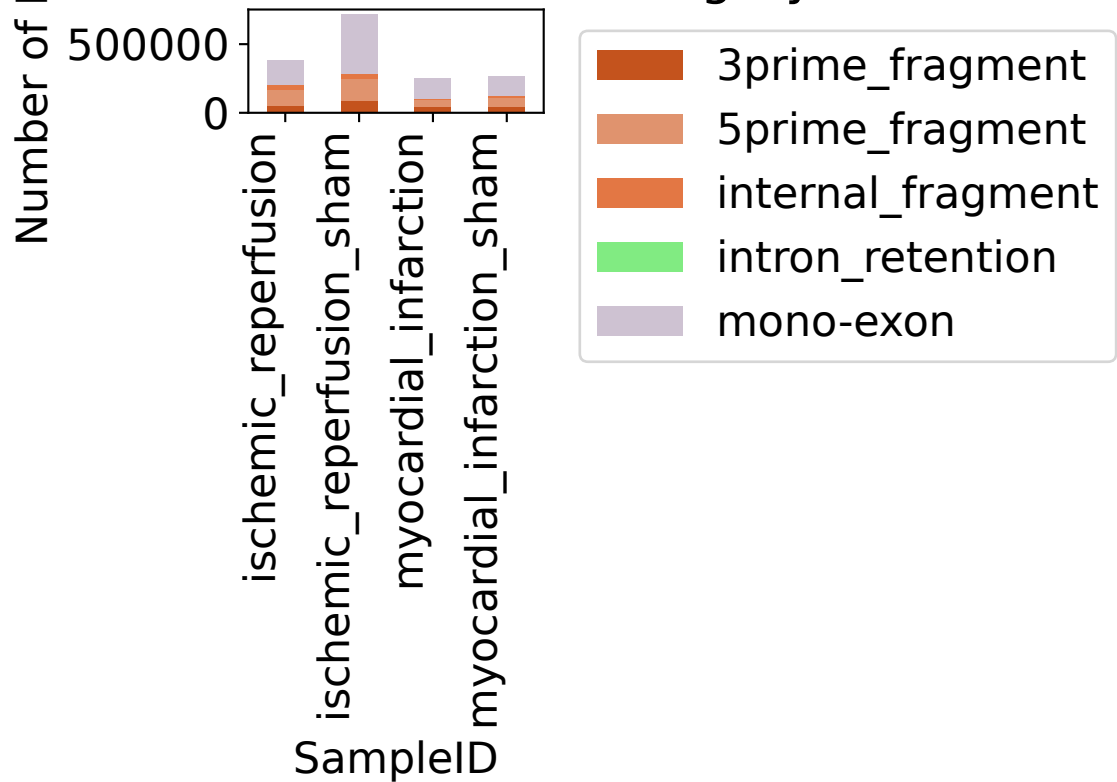
of Reads in Each subcategory - FSM



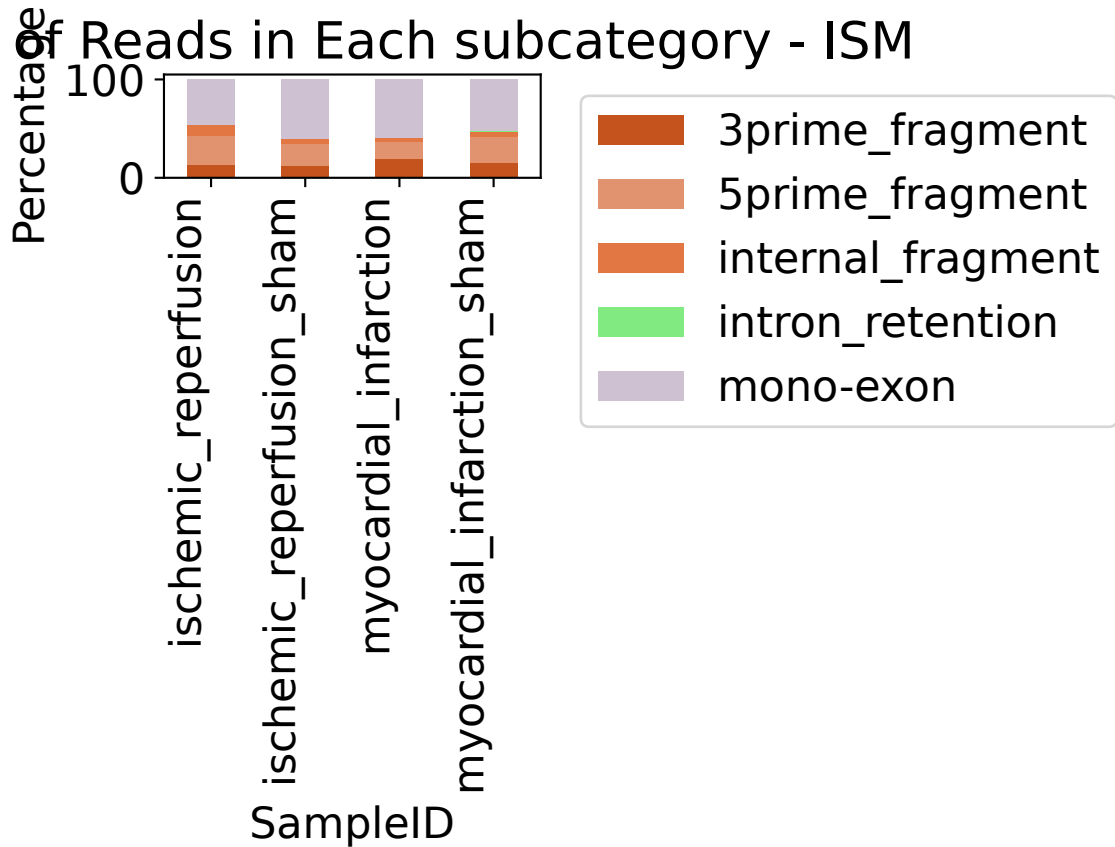
Percentage of Reads in Each subcategory - FSM



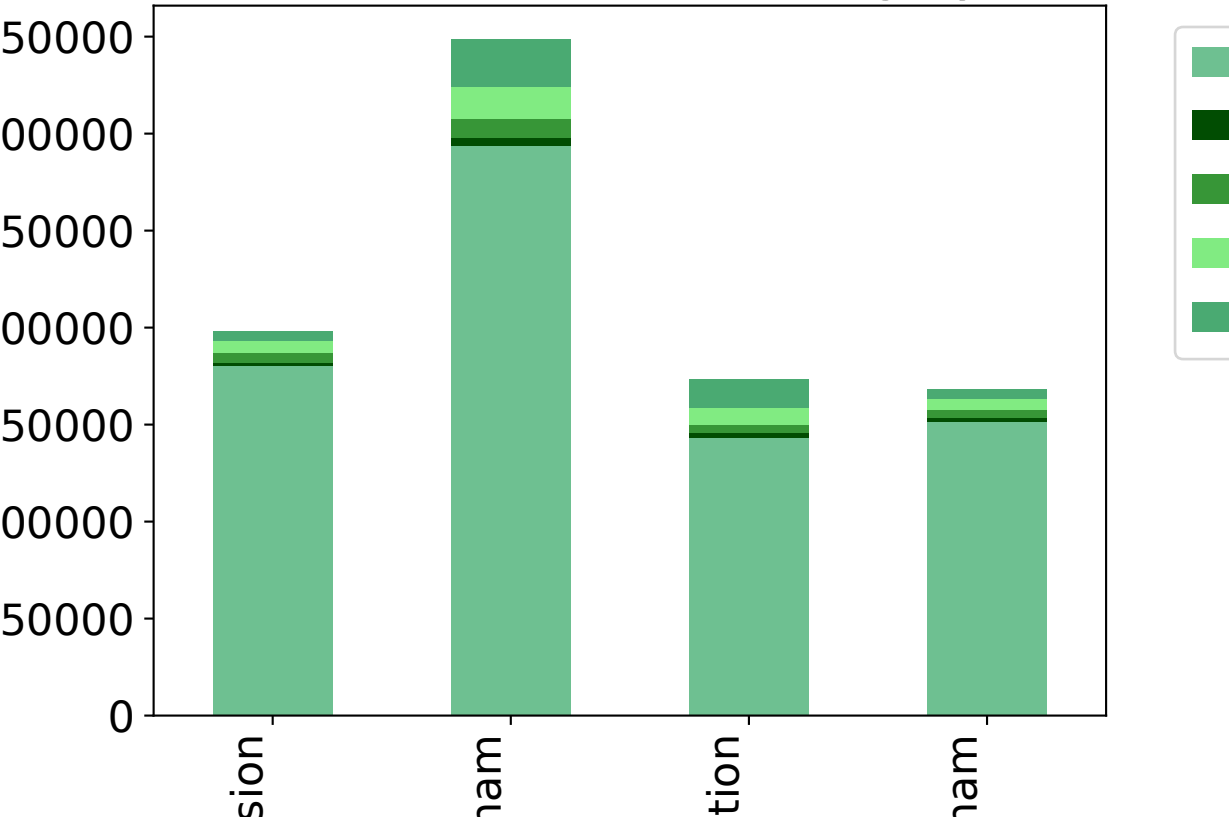
Number of Reads in Each subcategory - ISM



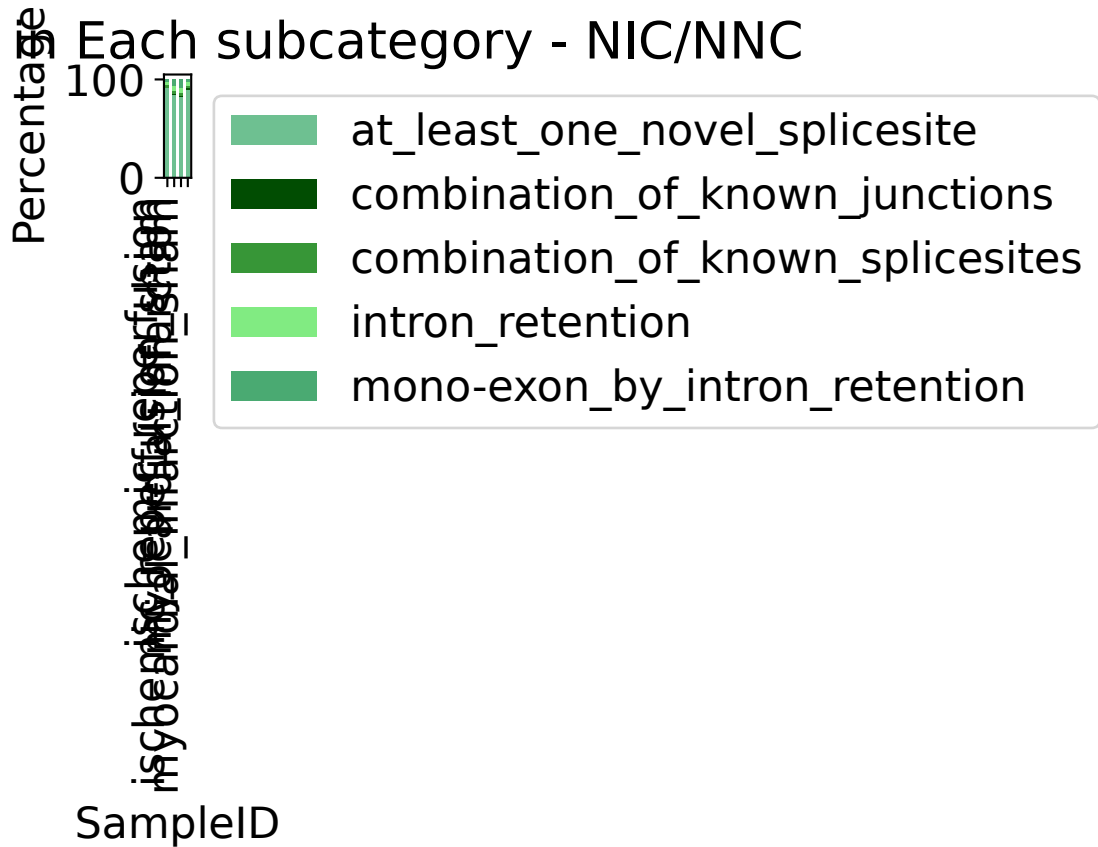
Percentage of Reads in Each subcategory - ISM

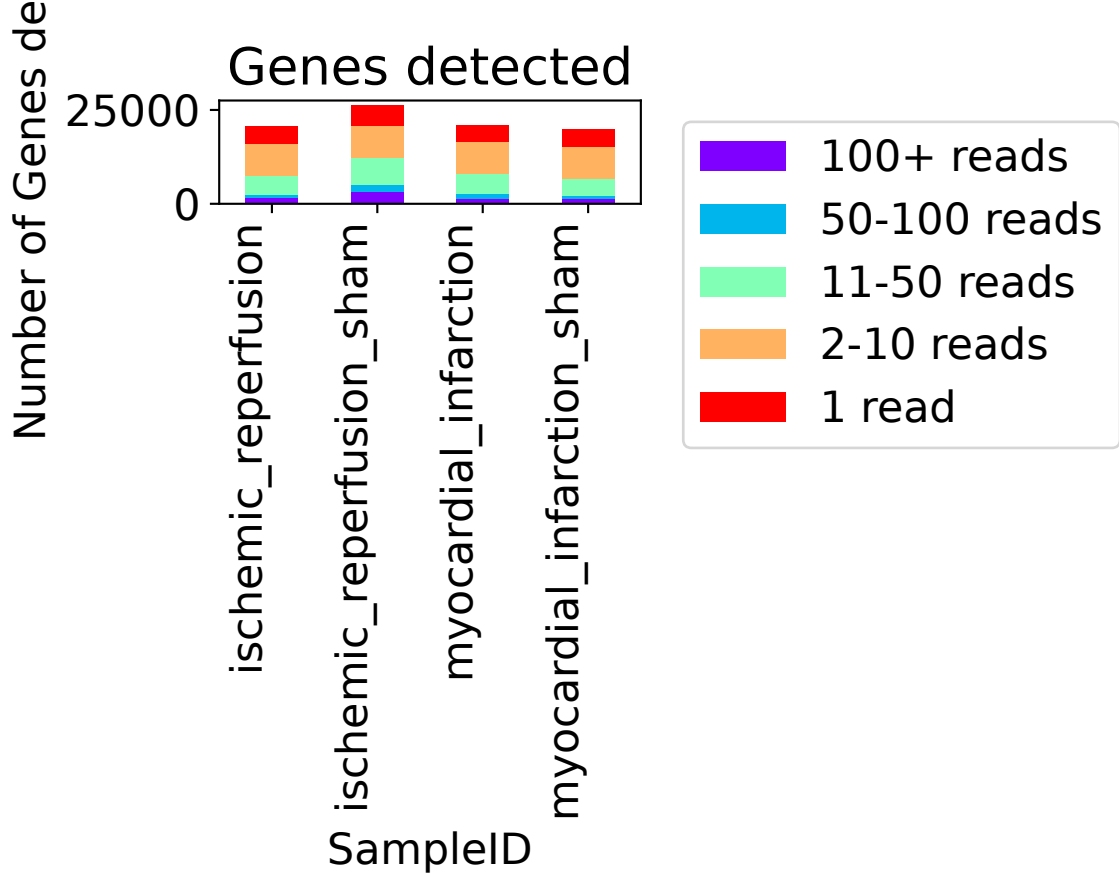


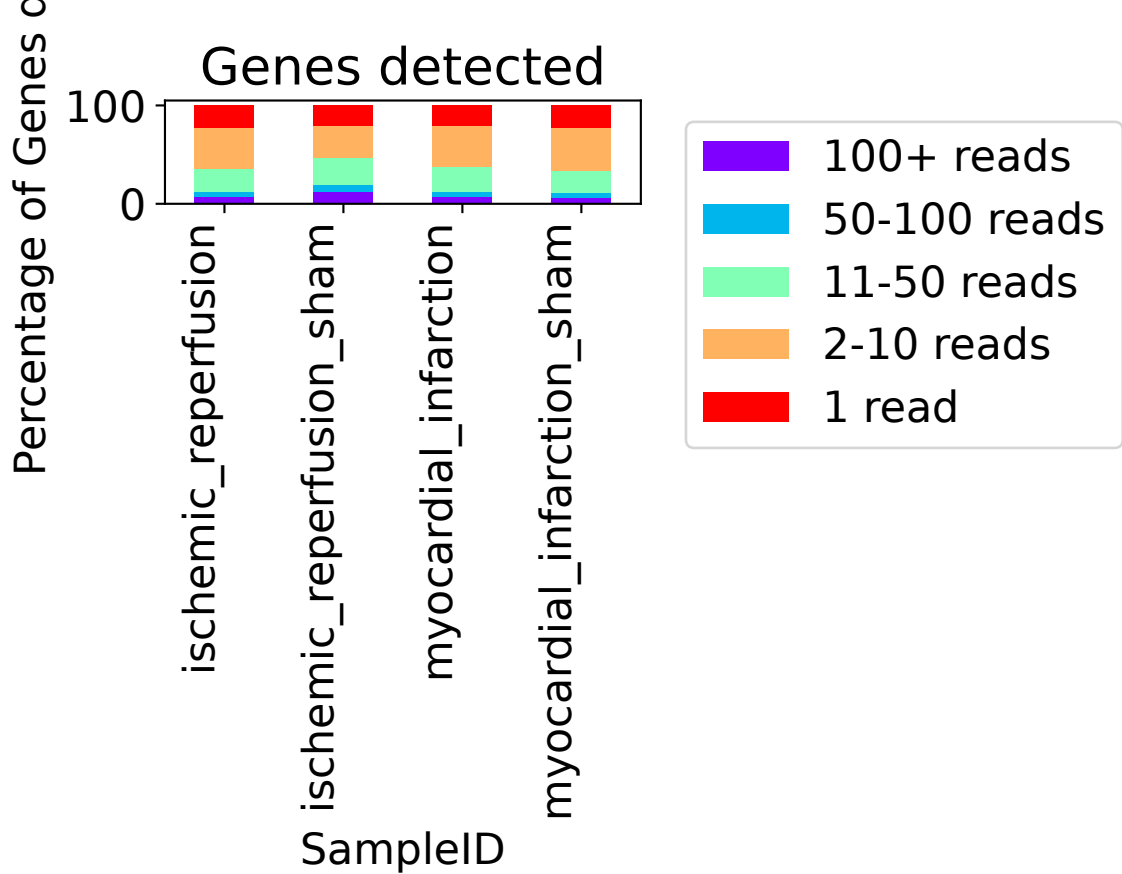
Number of Reads in Each subcategory - NIC/NNC



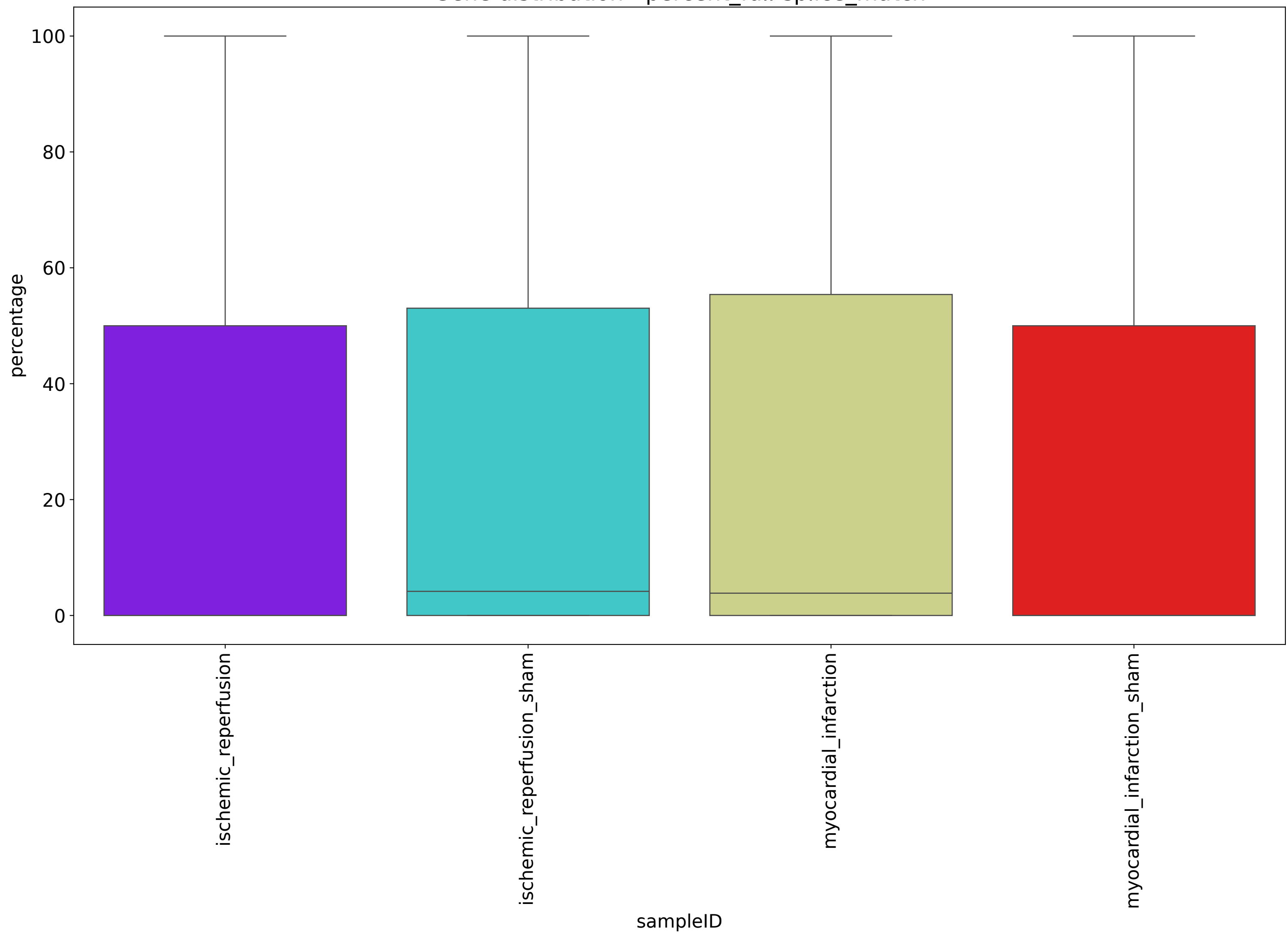
Each subcategory - NIC/NNC

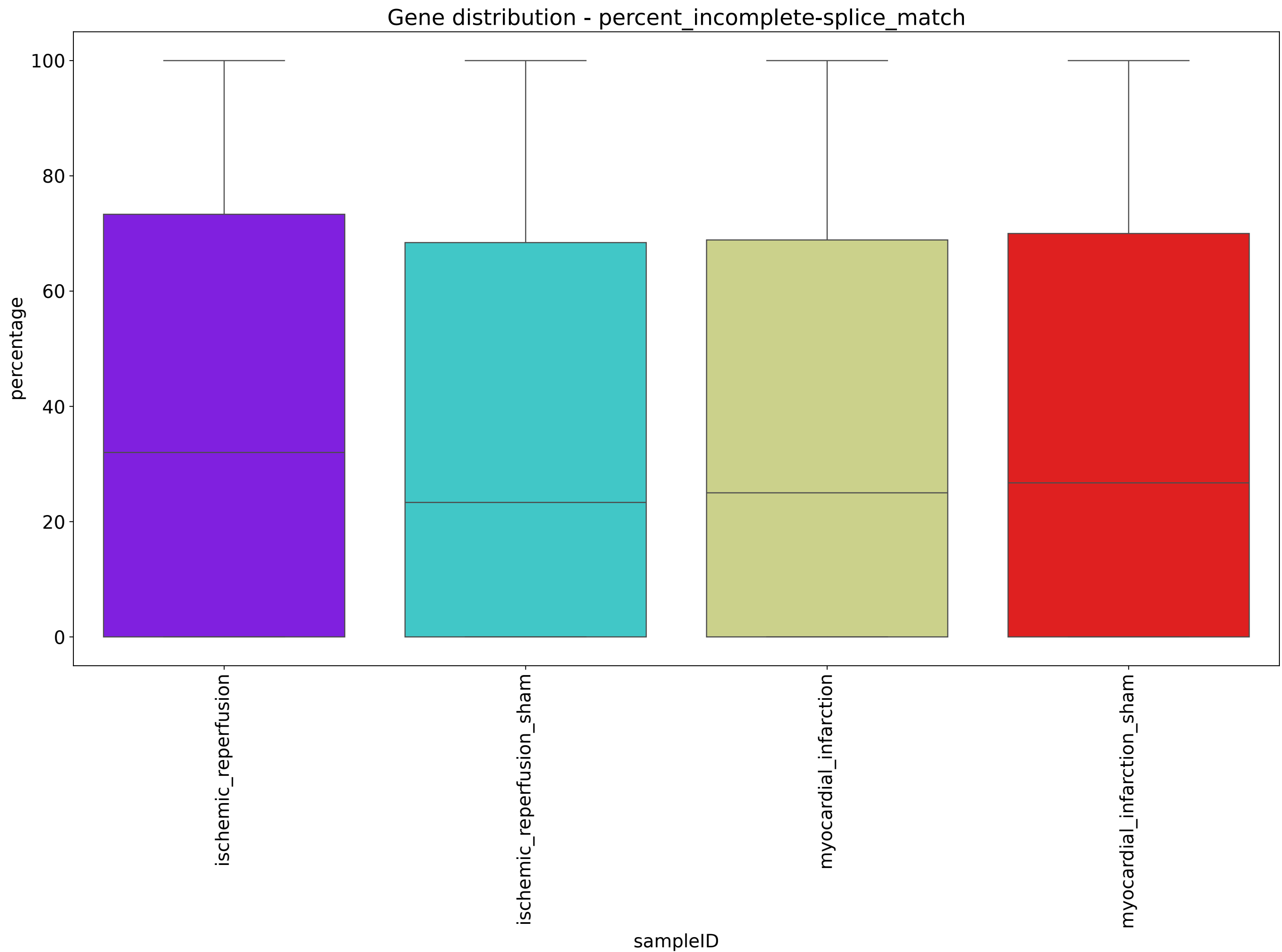




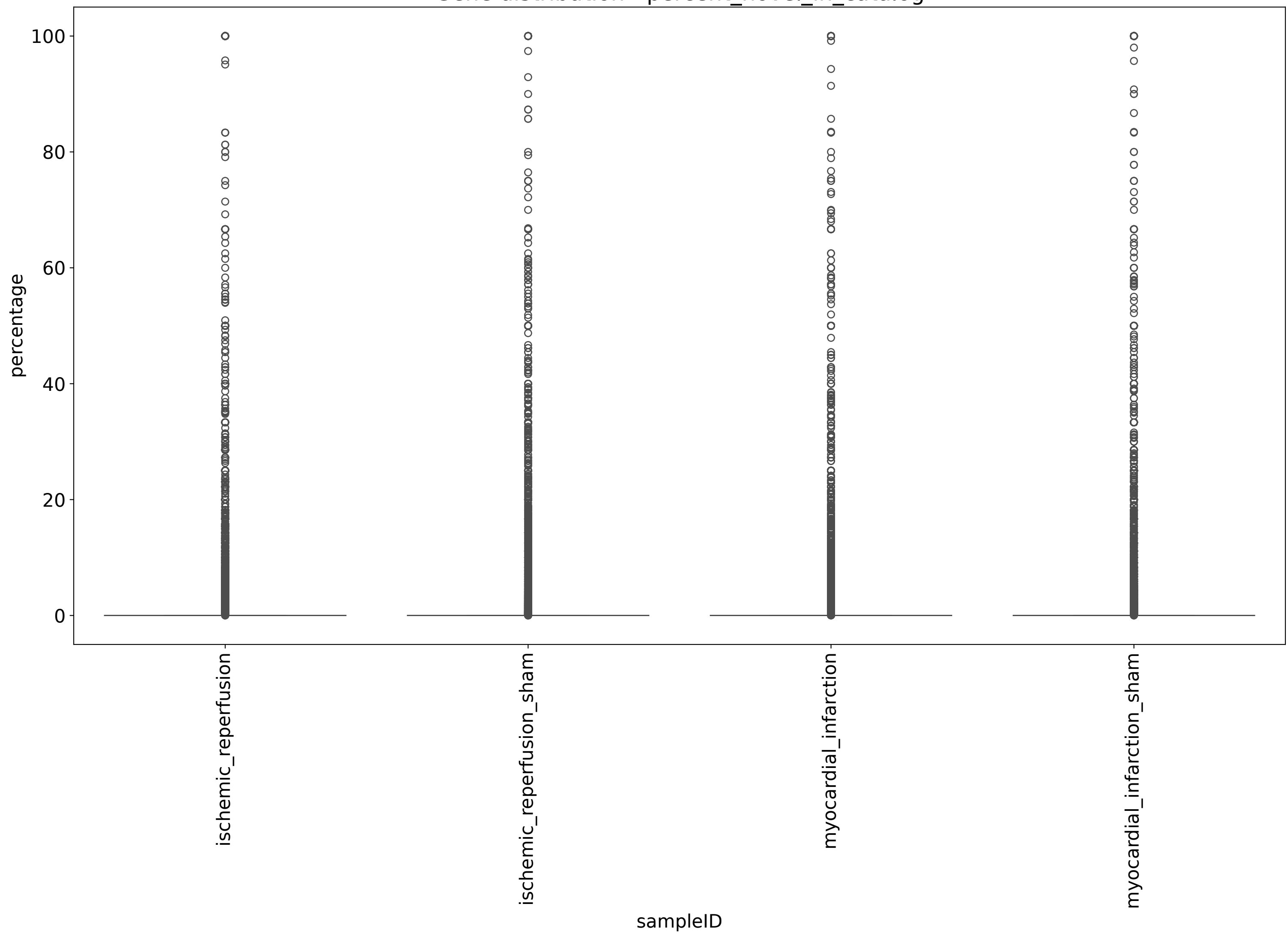


Gene distribution - percent_full-splice_match

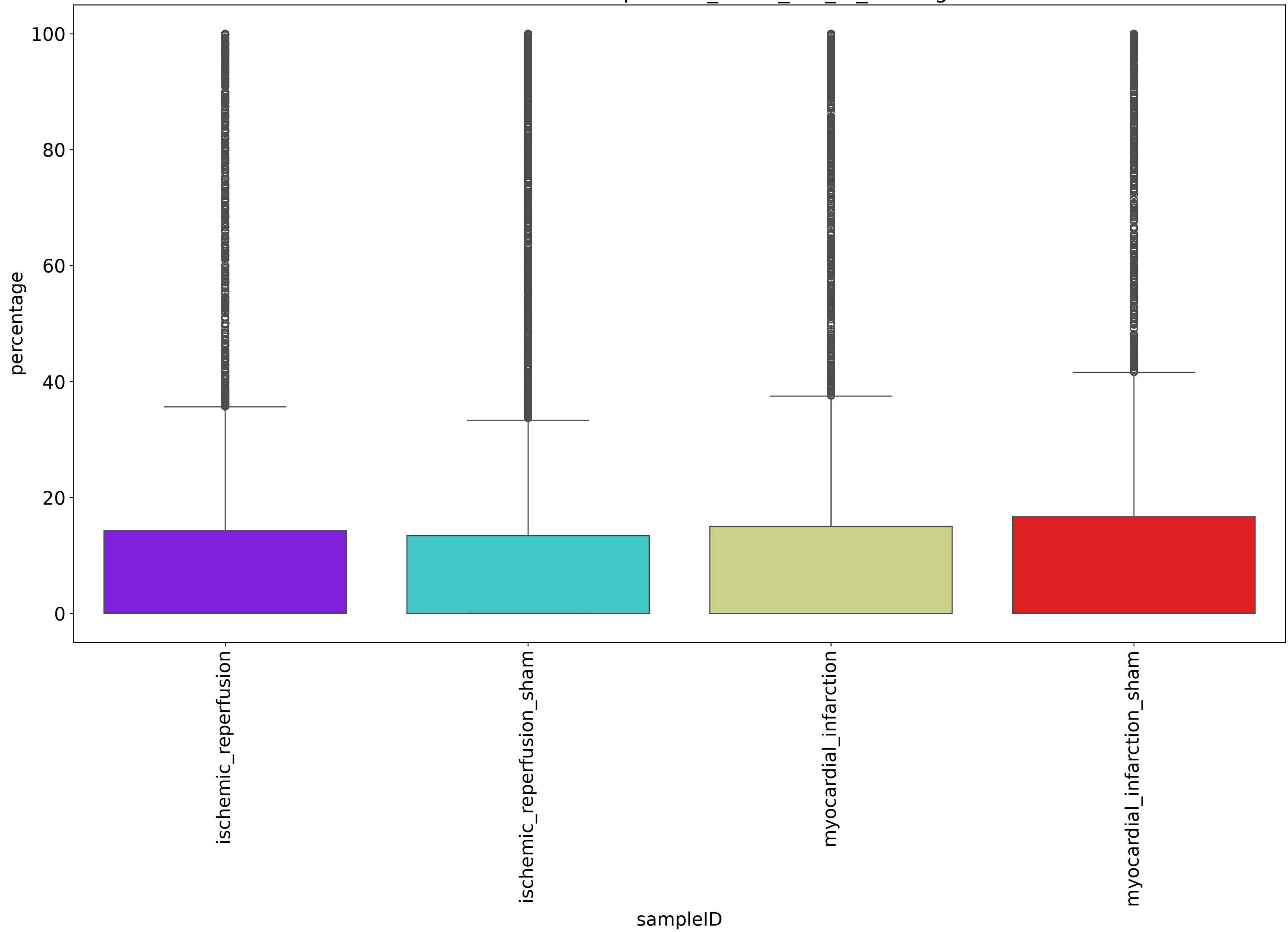




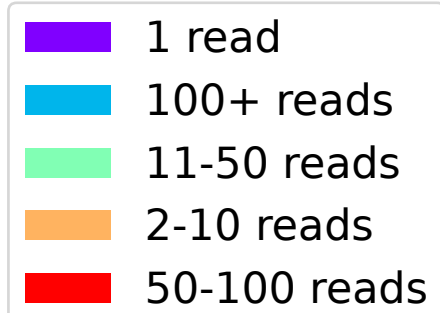
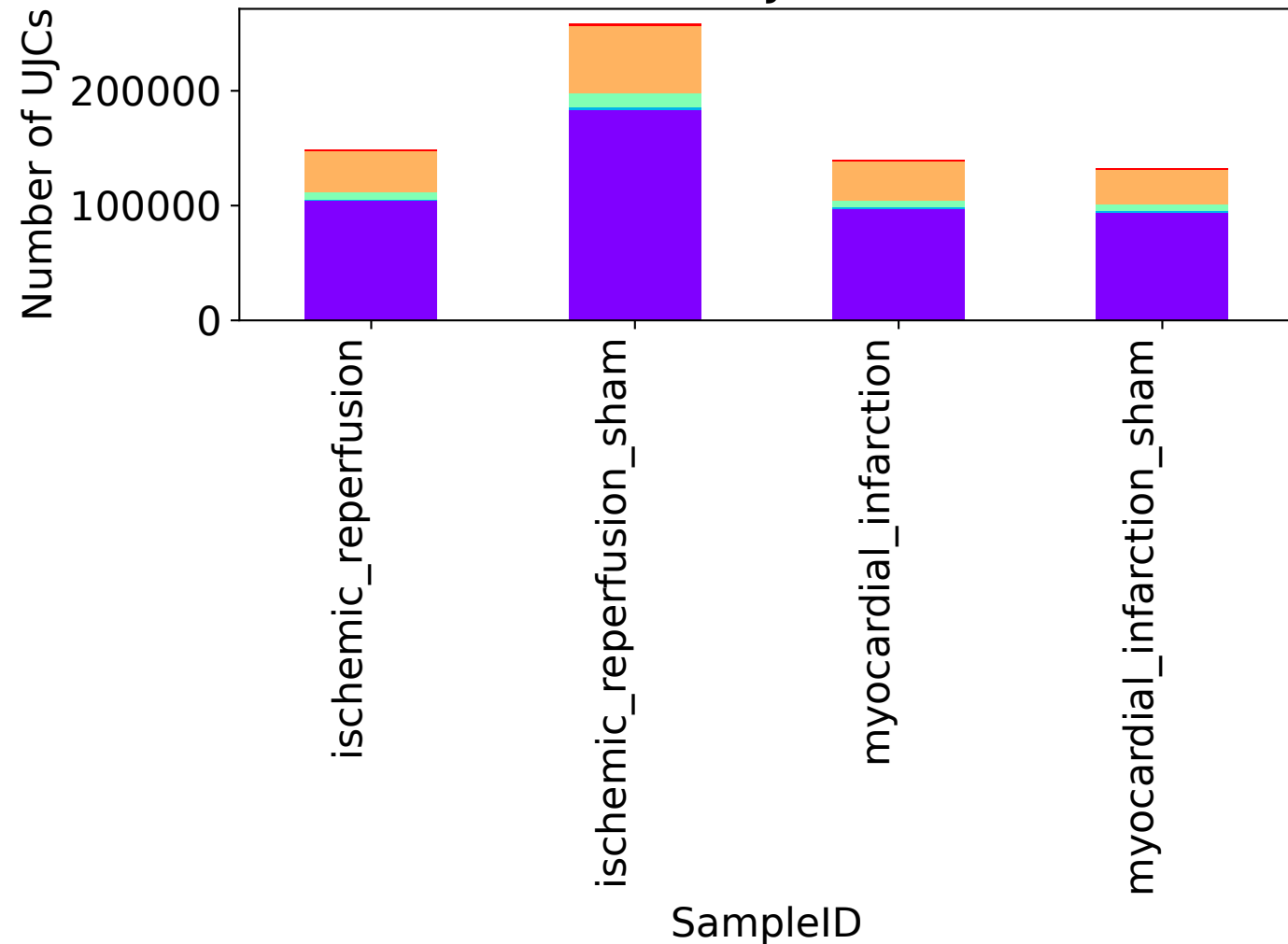
Gene distribution - percent_novel_in_catalog



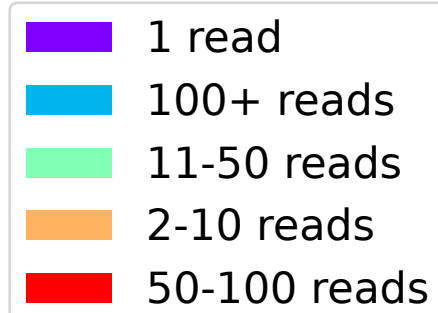
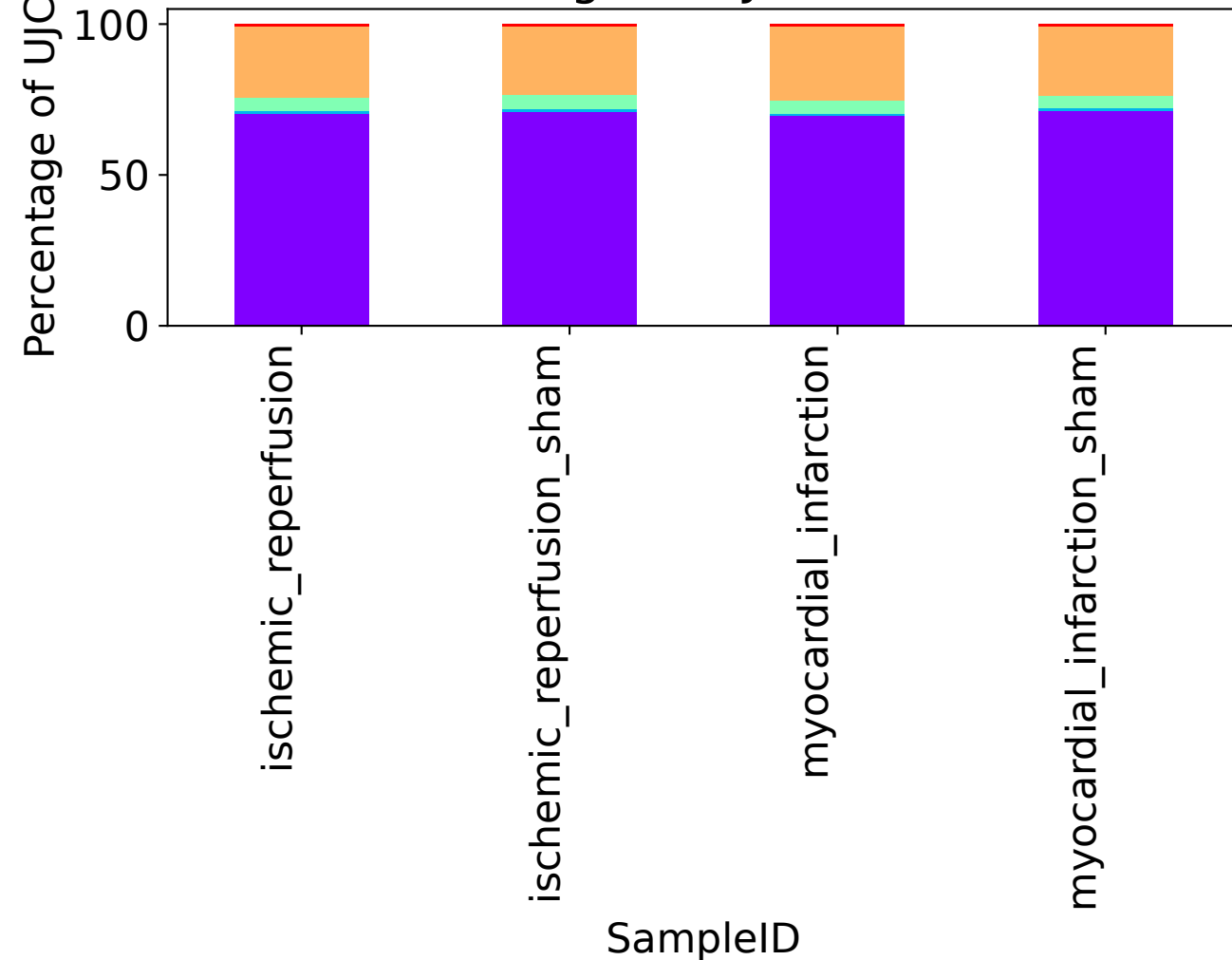
Gene distribution - percent_novel_not_in_catalog



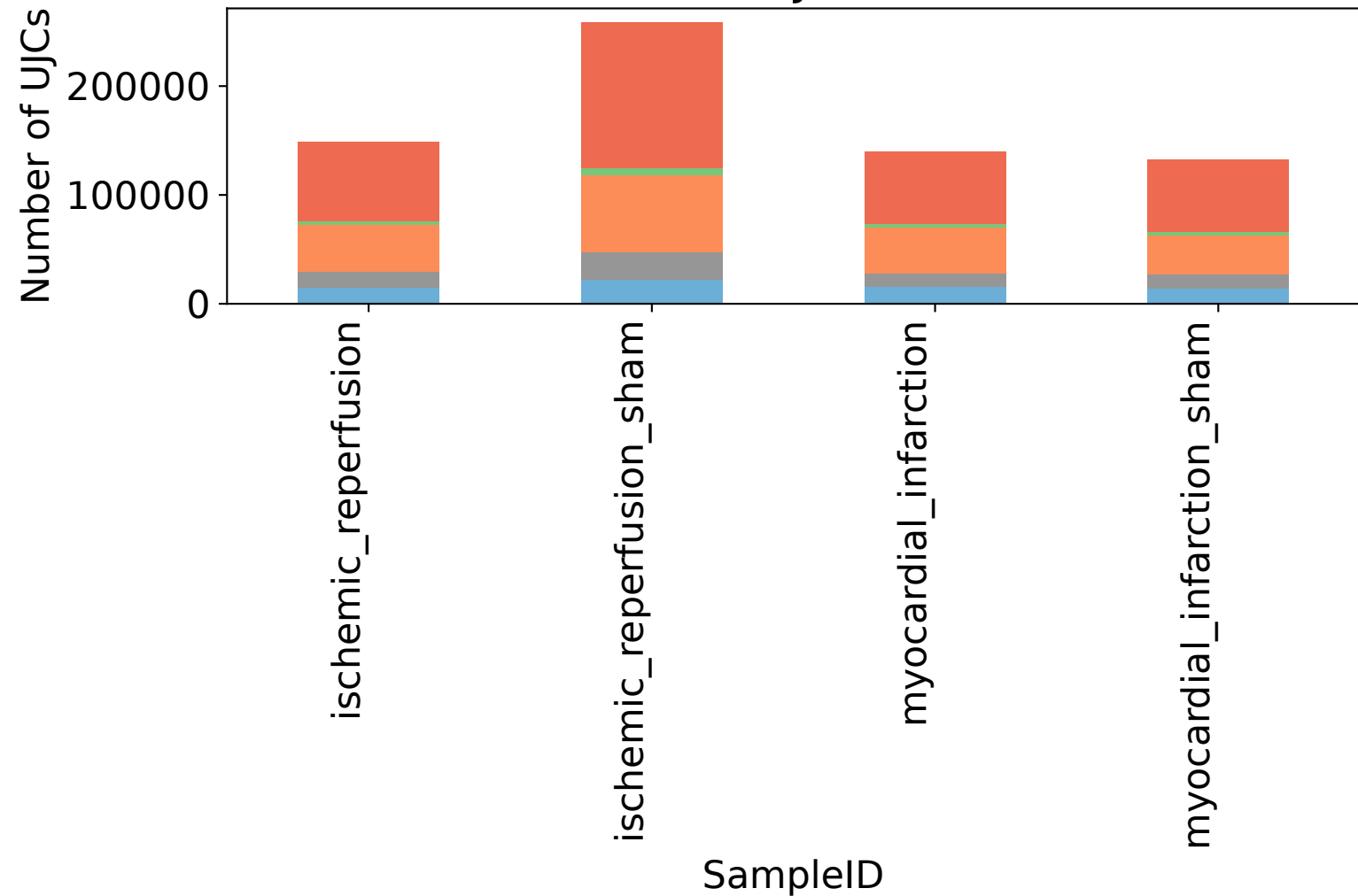
Number of UJCs detected



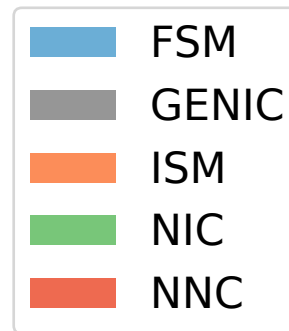
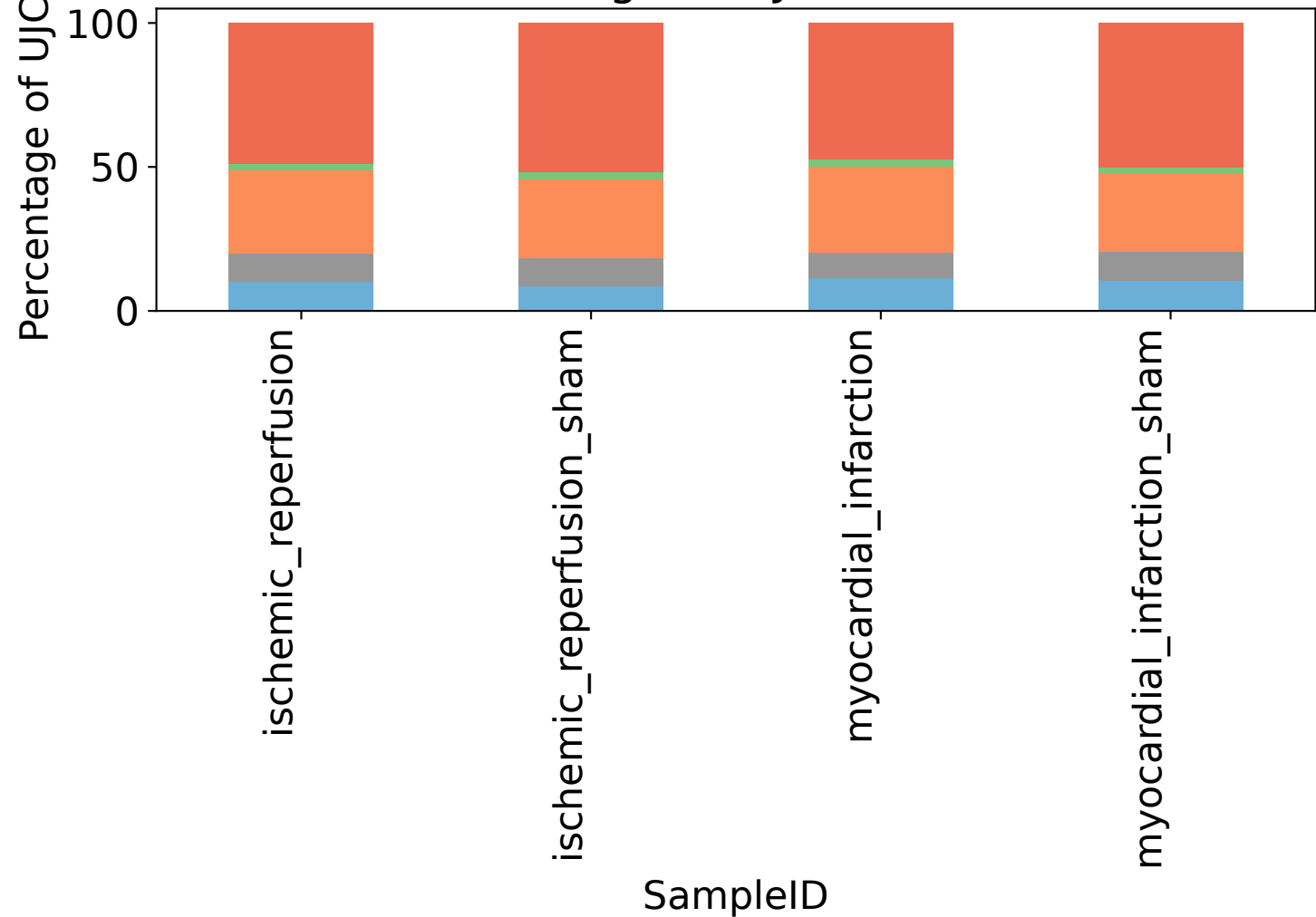
Percentage of UJCs detected



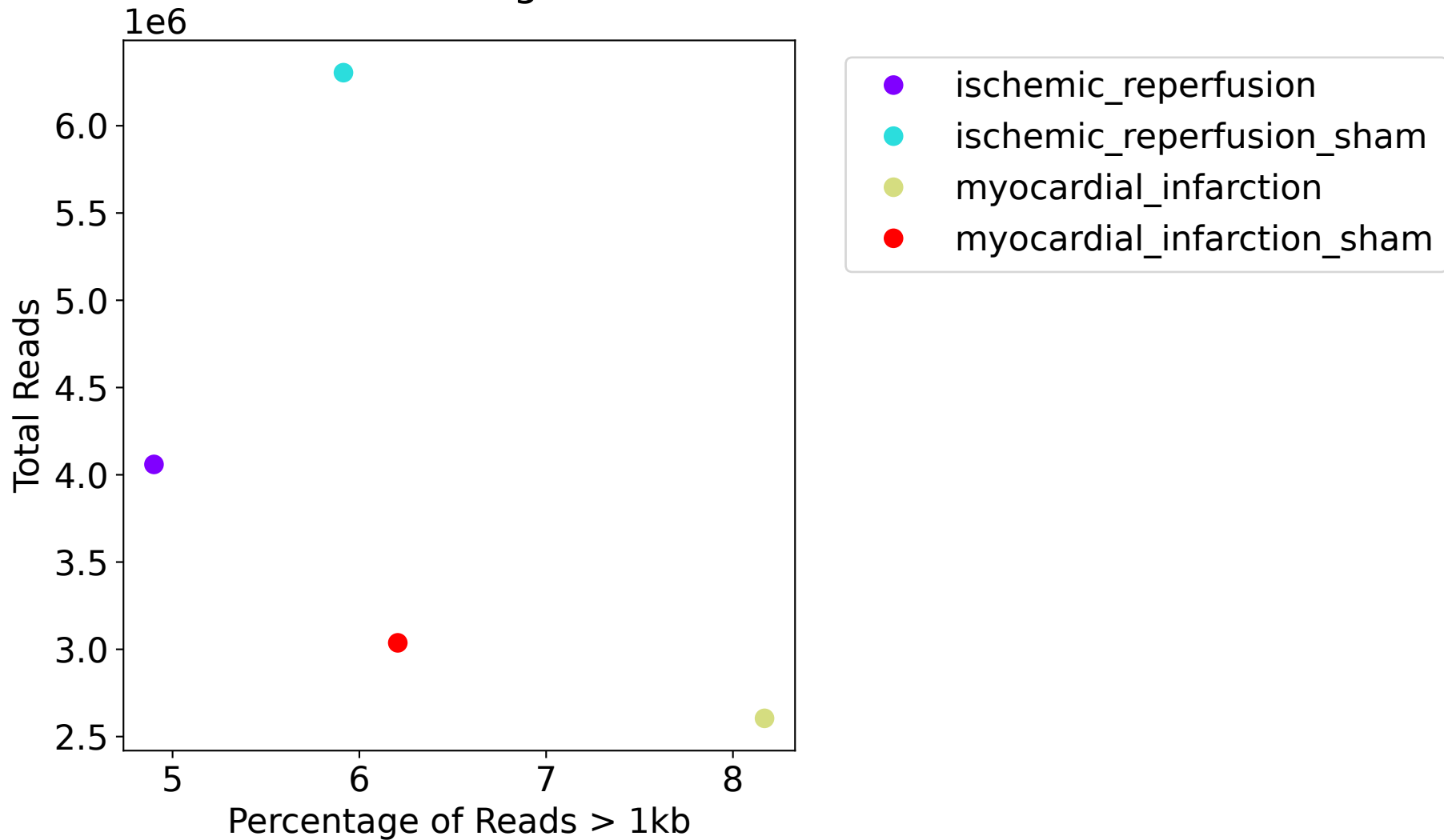
Number of UJCs detected

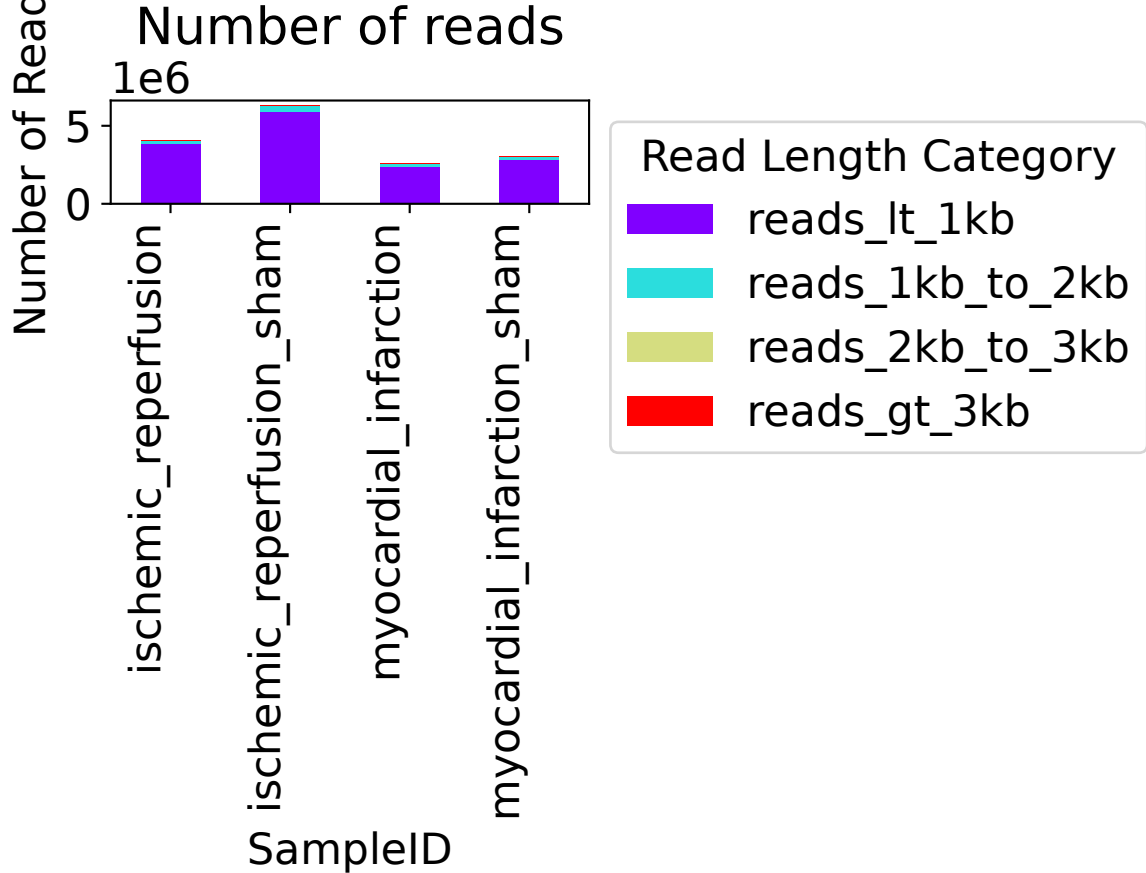


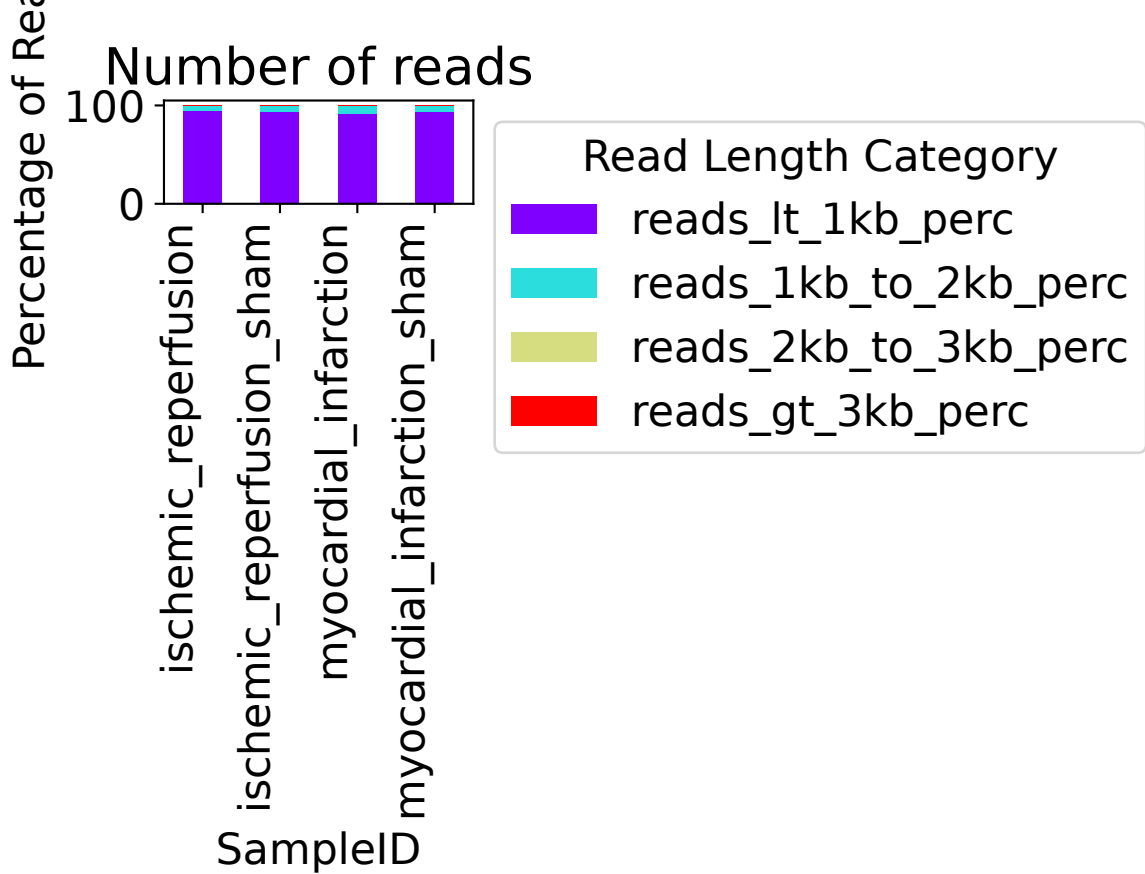
Percentage of UJCs detected



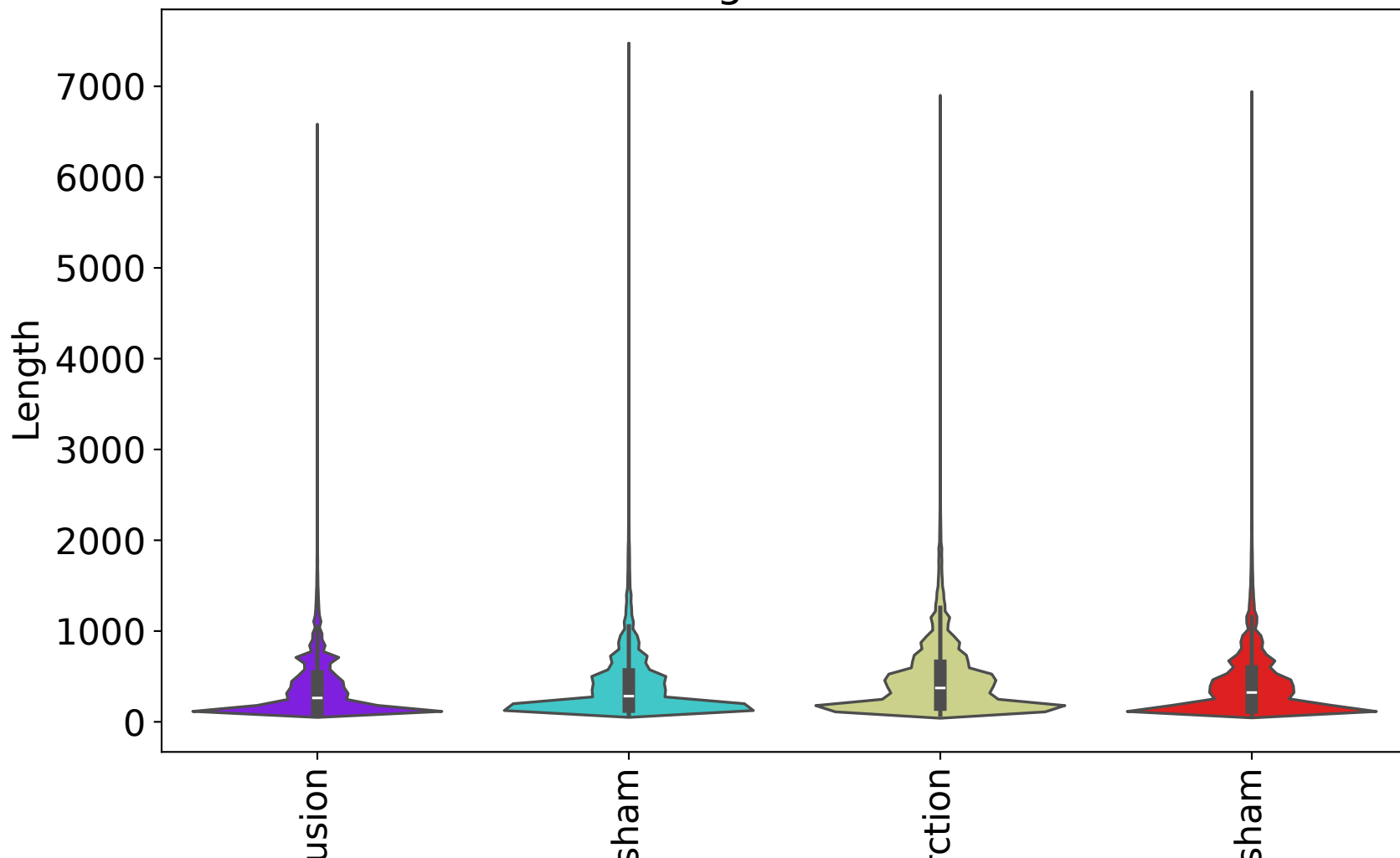
Total Reads vs Percentage of Reads > 1kb



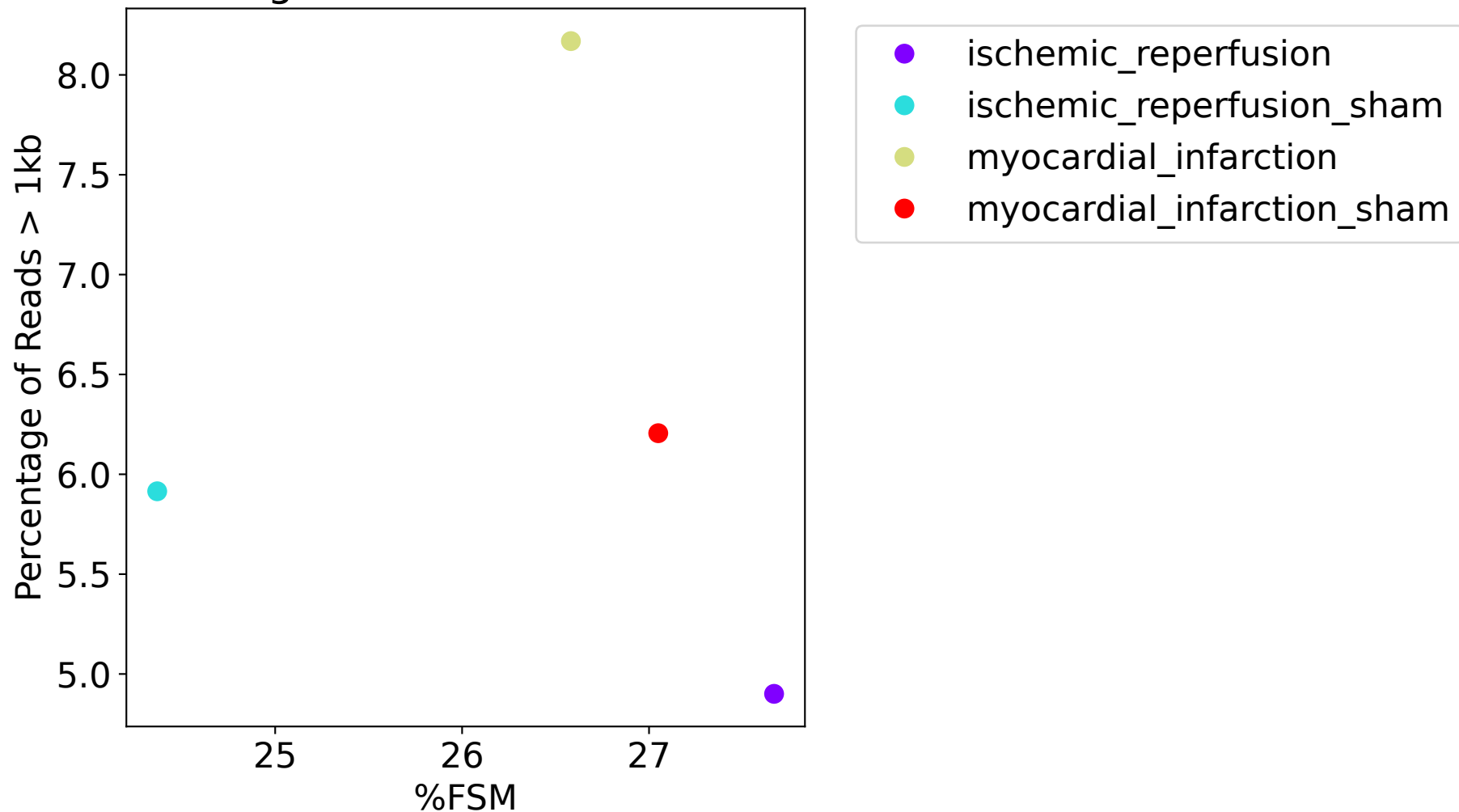




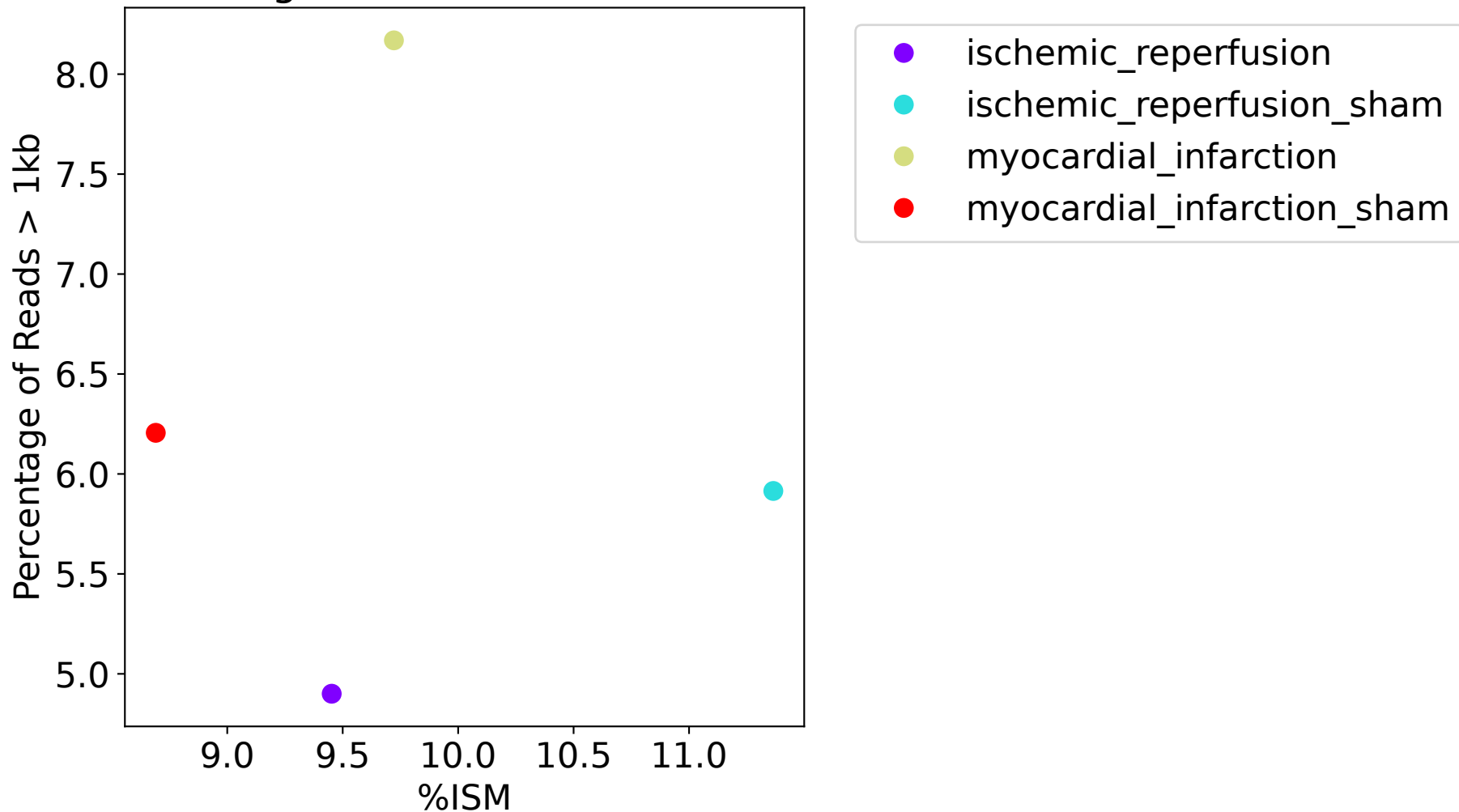
Read Length Distribution



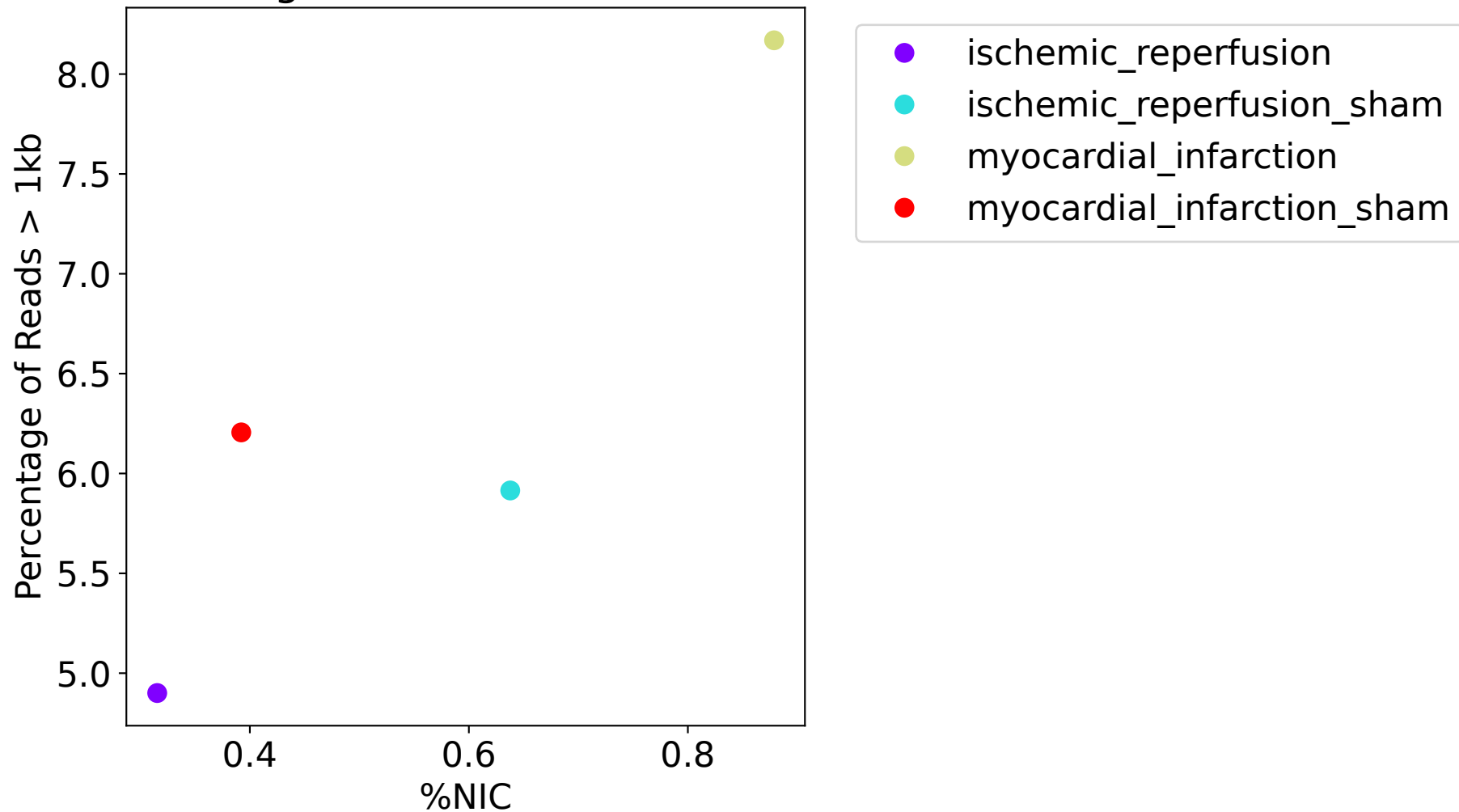
Percentage of Reads > 1kb vs %FSM



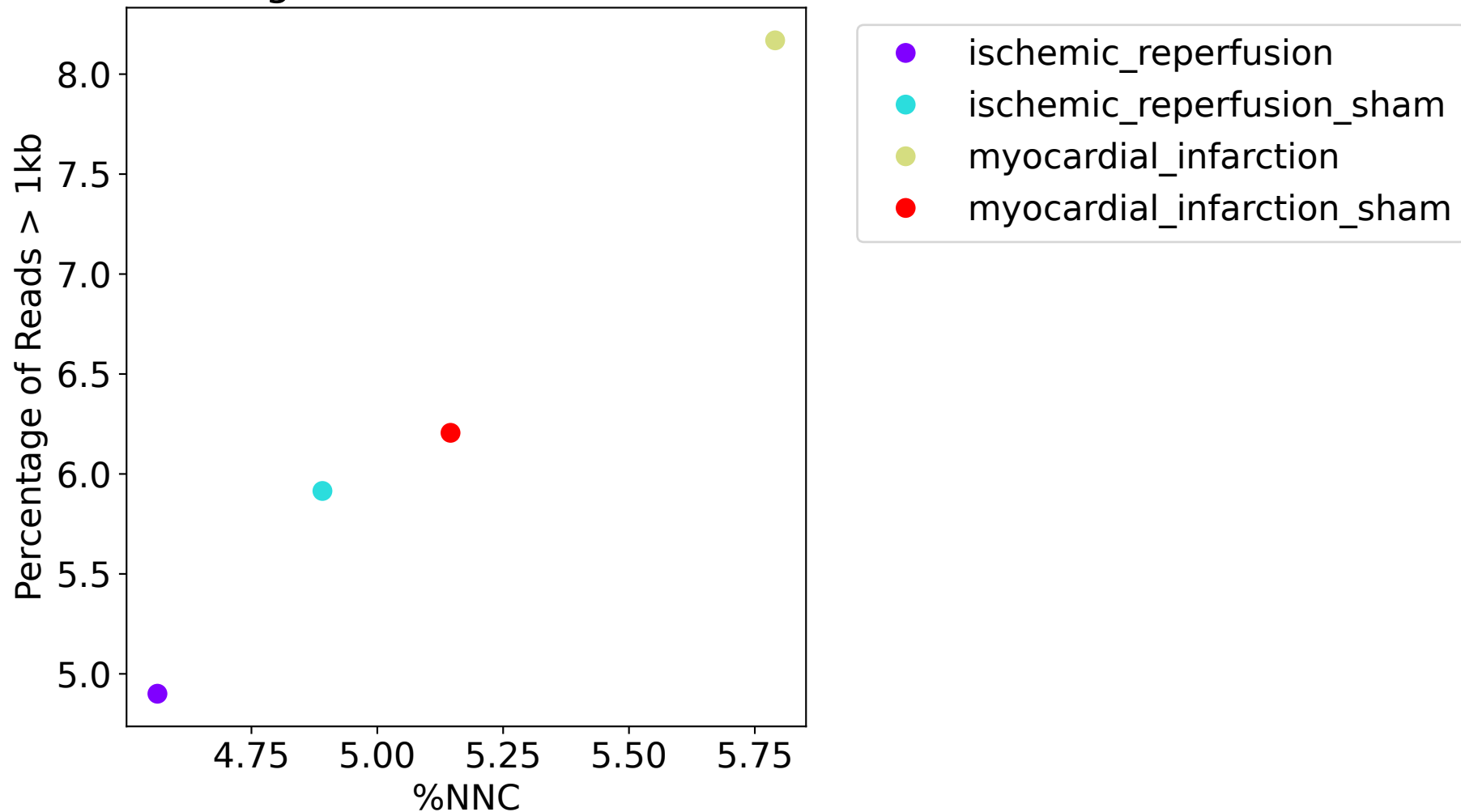
Percentage of Reads > 1kb vs %ISM



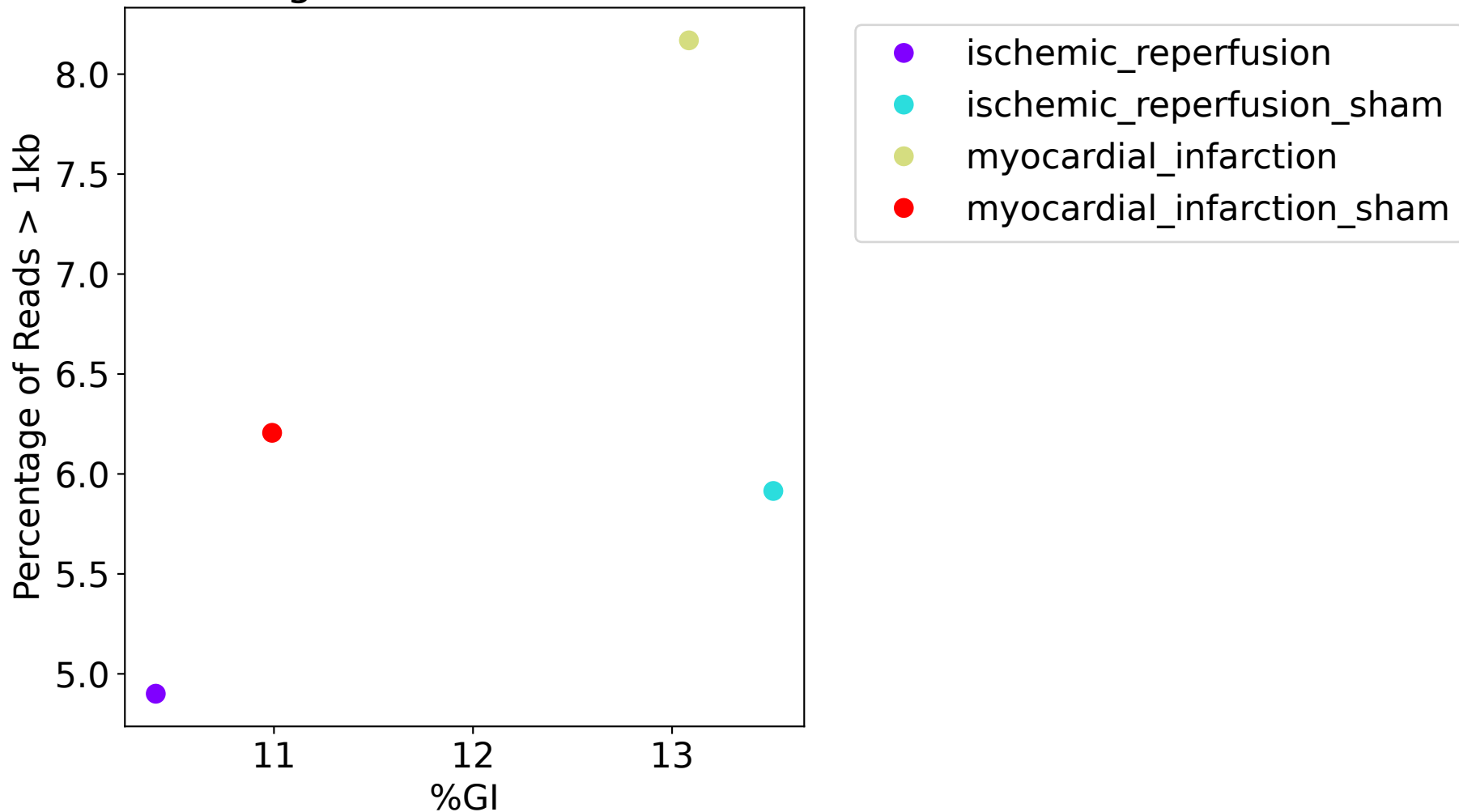
Percentage of Reads > 1kb vs %NIC



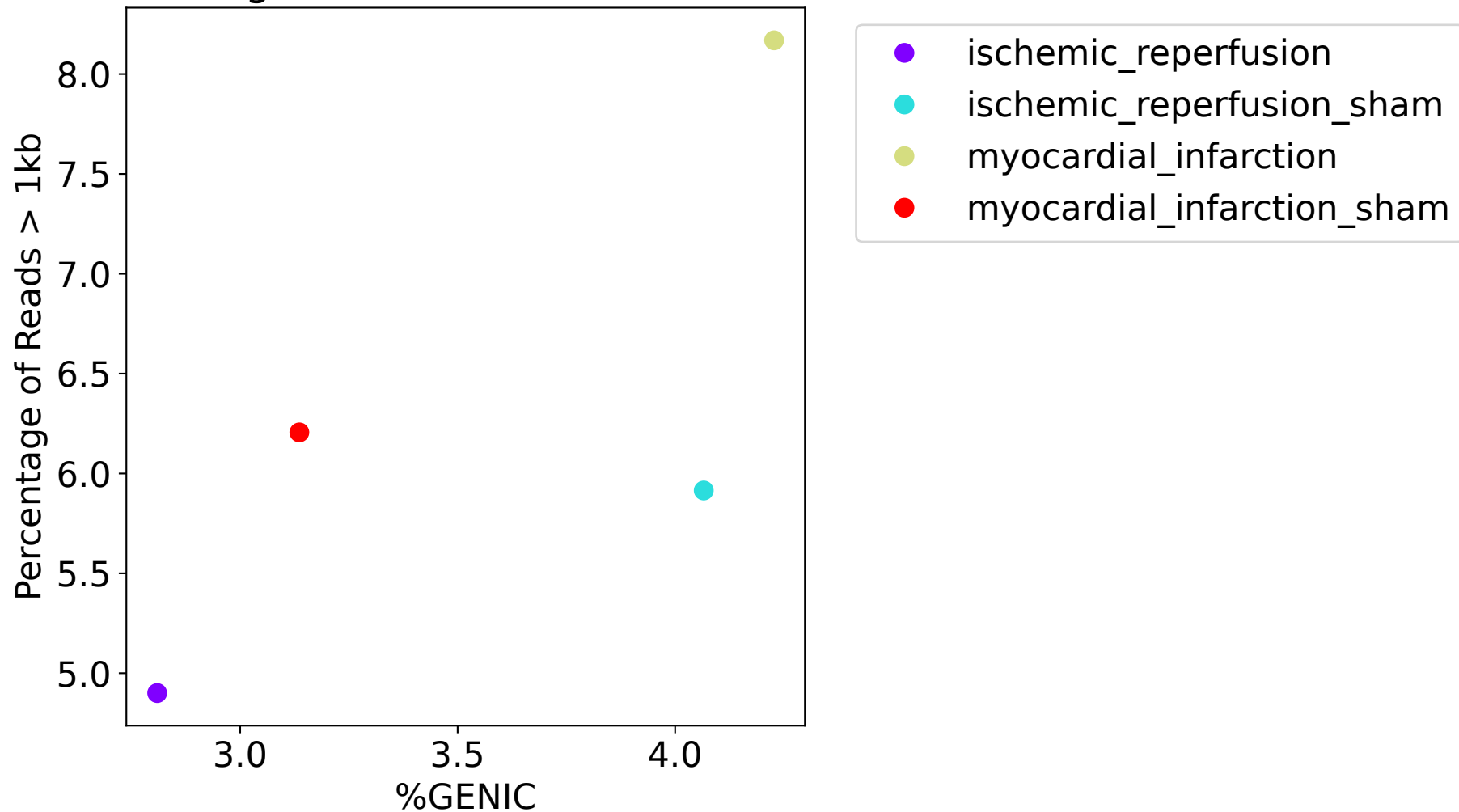
Percentage of Reads > 1kb vs %NNC



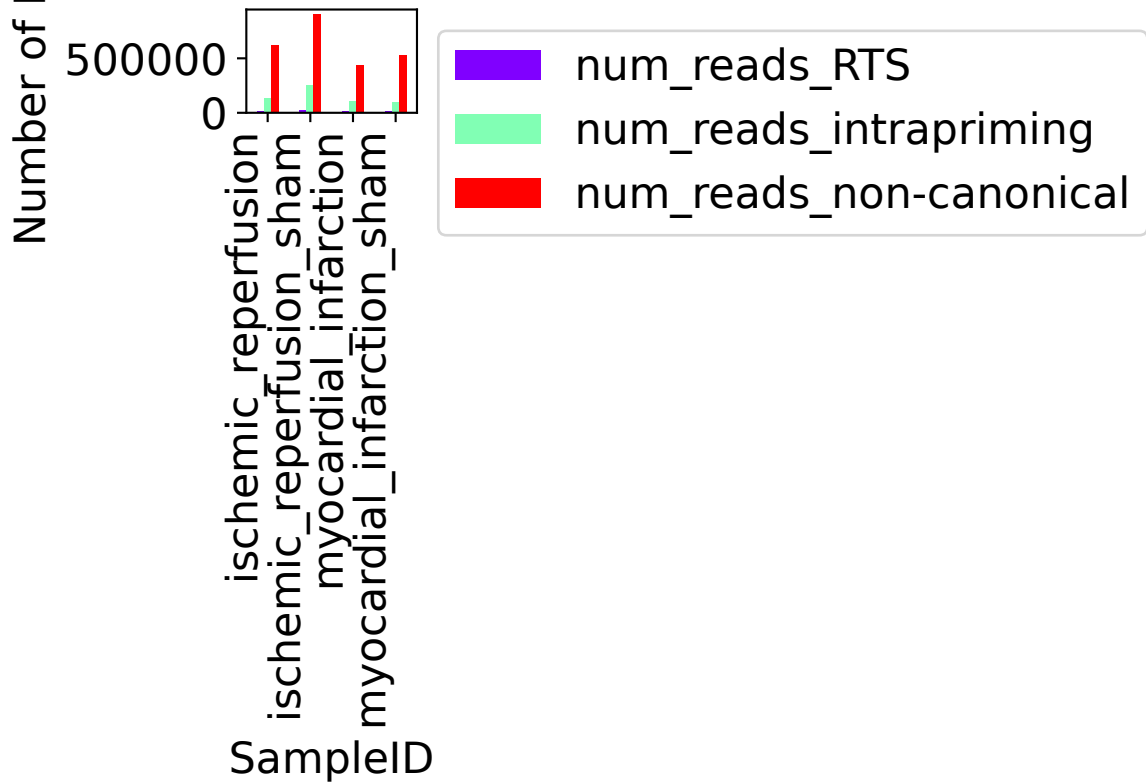
Percentage of Reads > 1kb vs %GI



Percentage of Reads > 1kb vs %GENIC



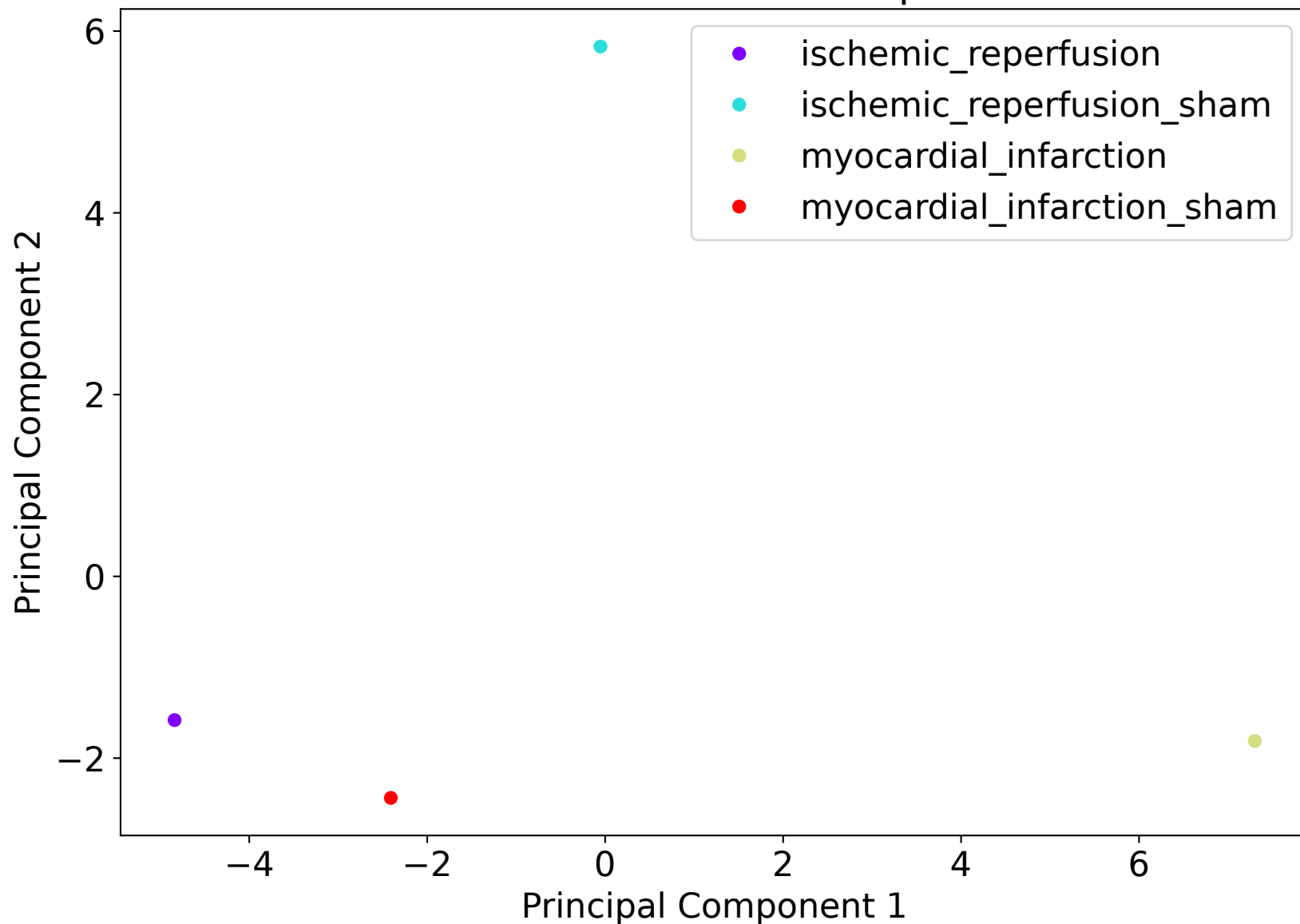
Number of Artefact reads



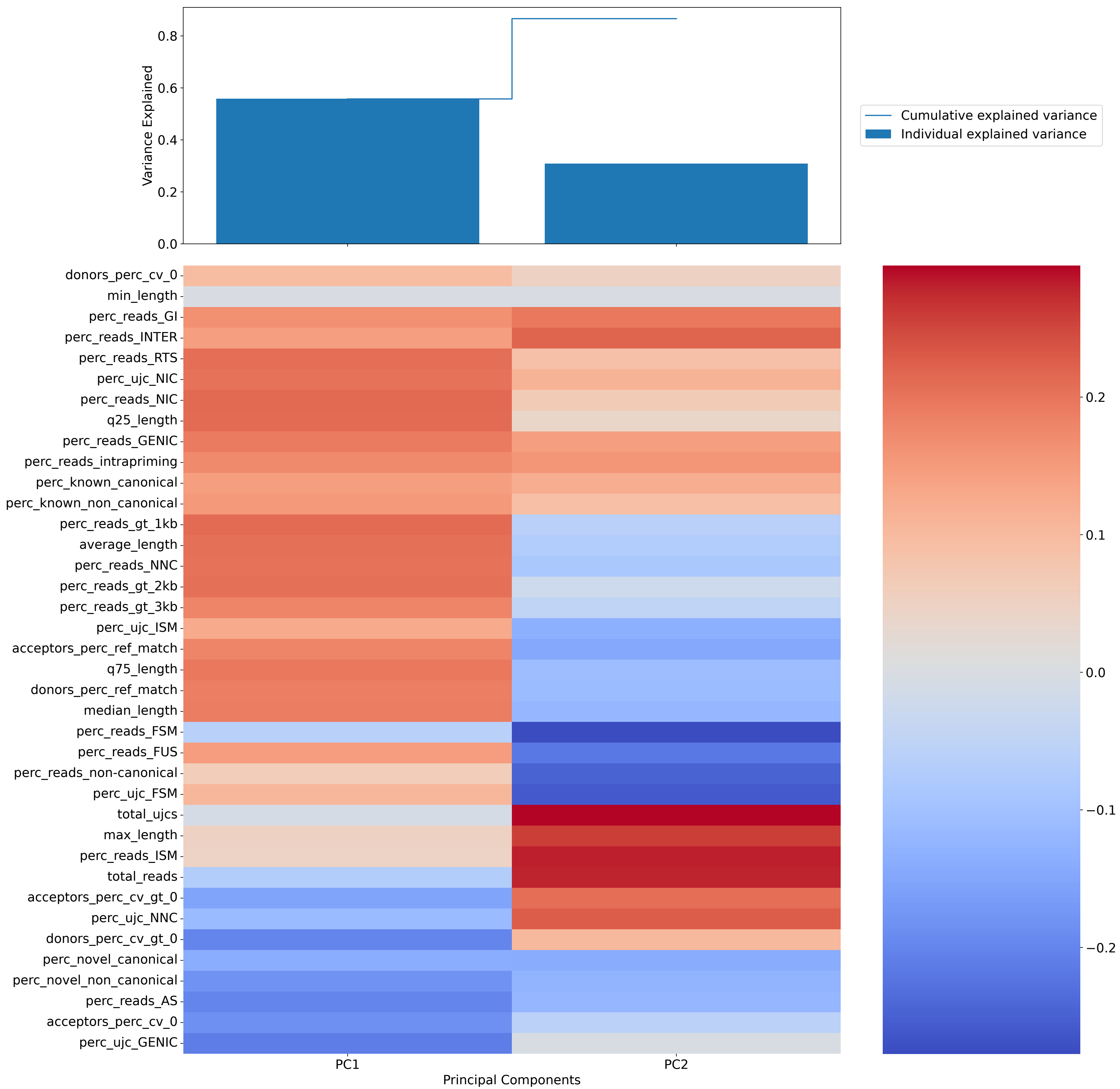
Percent Artefact reads



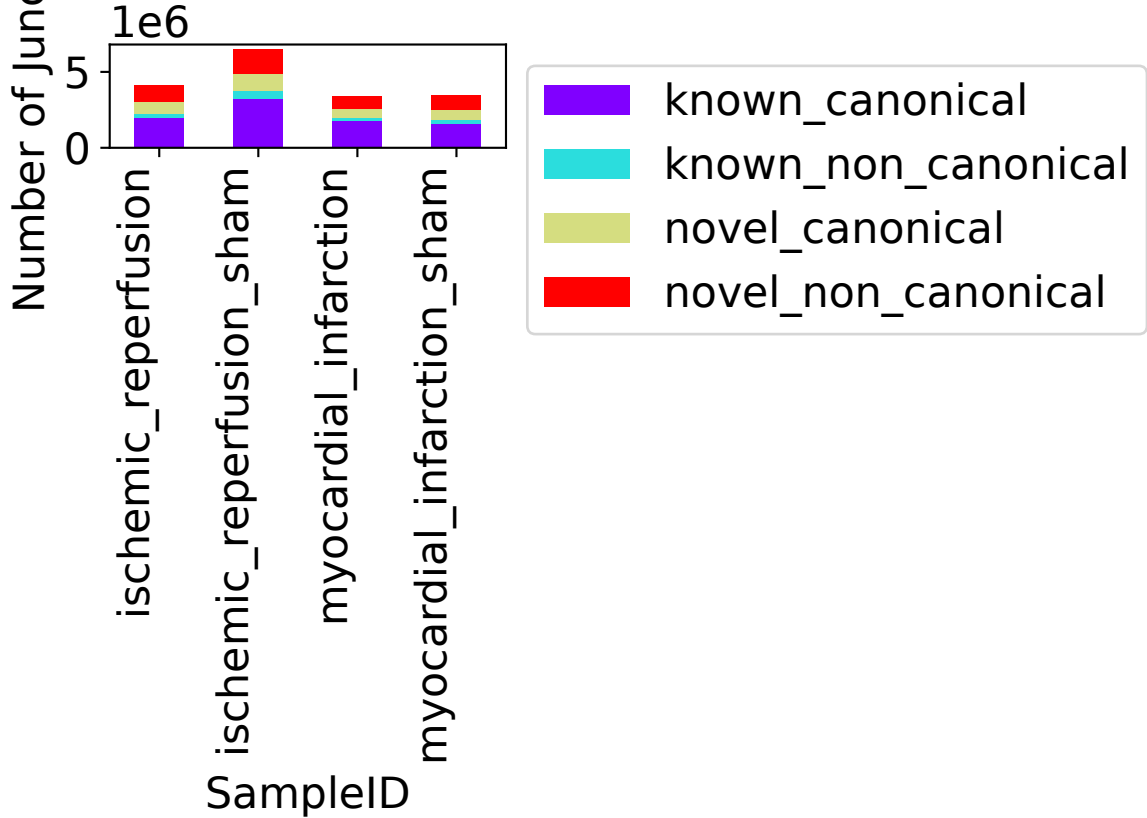
PCA Plot Based on sampleID



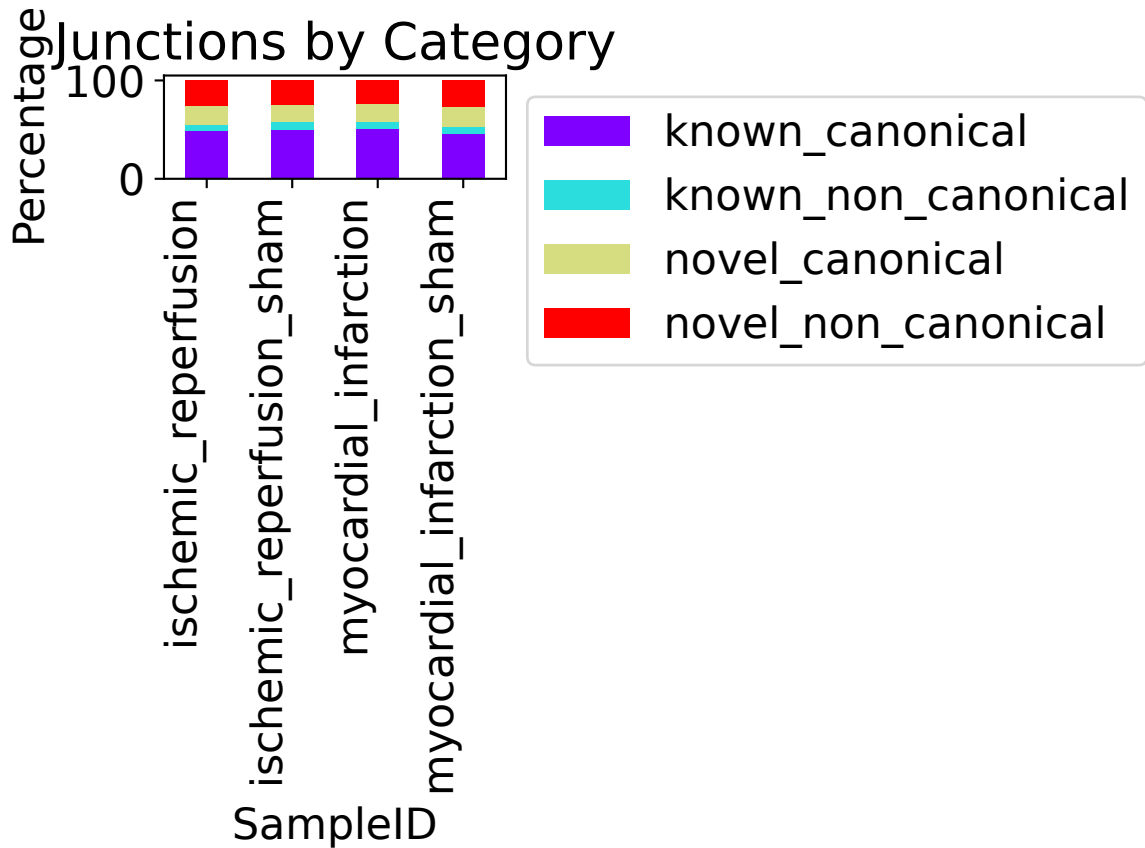
Variance and Heatmap of PC loadings

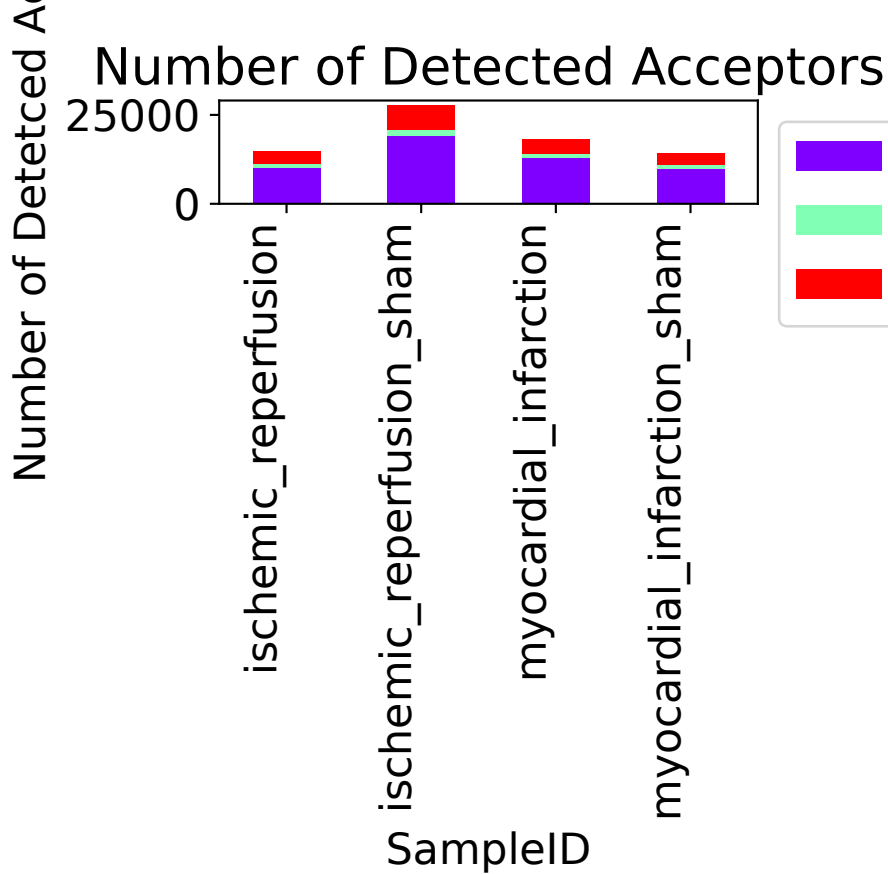


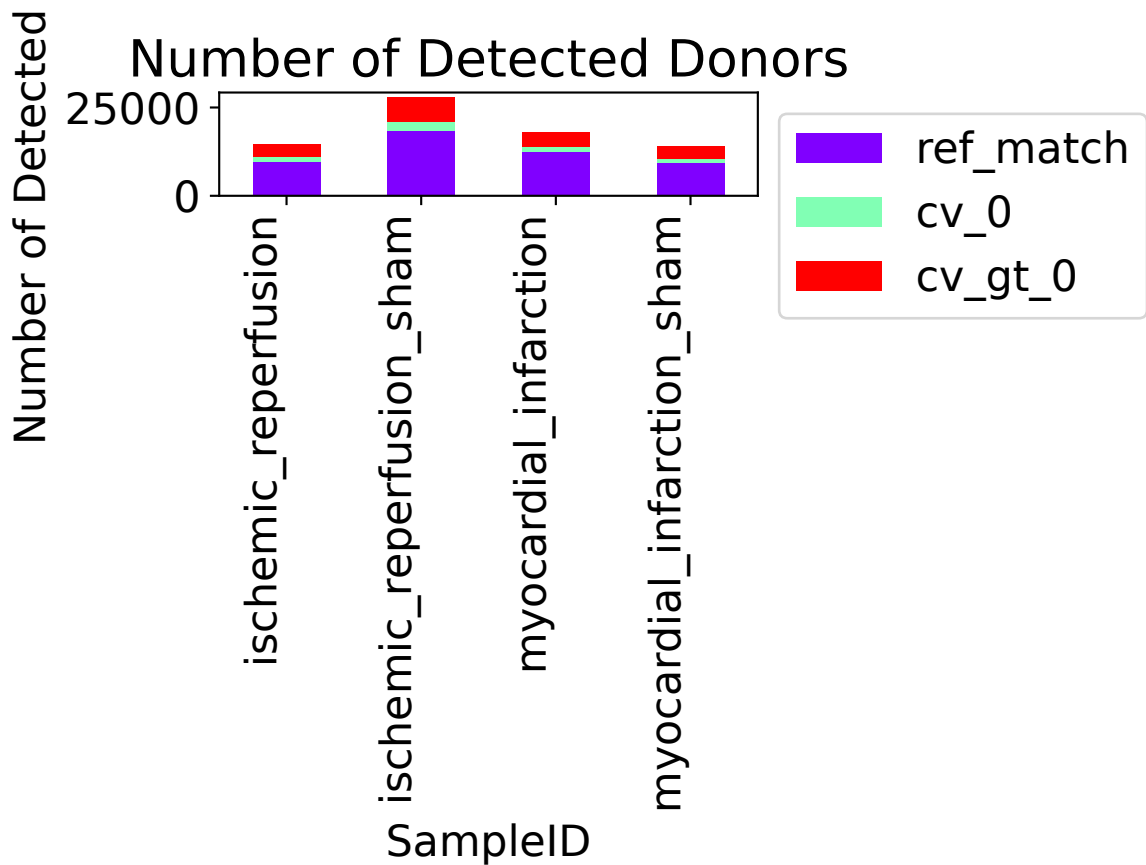
junctions by Category



Junctions by Category







Percentage of Detected Acceptors

